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OM protein - protein search, using sw model

Run on: January 9, 2002, 15:01:13 ; Search time 83.2 Seconds  
(without alignments)  
16.025 Million cell updates/sec

Title: US-09-828-000-6

Perfect score: 96

Sequence: 1 VIFNYKKNVLINKDIRC 18

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 522463 seqs, 74073290 residues

Total number of hits satisfying chosen parameters: 522463

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A\_Geneseq\_1101.\*

- 1: /SIDS8/gcgdata/geneseq/geneseqp/AA1980.DAT.\*
- 2: /SIDS8/gcgdata/geneseq/geneseqp/AA1981.DAT.\*
- 3: /SIDS8/gcgdata/geneseq/geneseqp/AA1982.DAT.\*
- 4: /SIDS8/gcgdata/geneseq/geneseqp/AA1983.DAT.\*
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- 11: /SIDS8/gcgdata/geneseq/geneseqp/AA1990.DAT.\*
- 12: /SIDS8/gcgdata/geneseq/geneseqp/AA1991.DAT.\*
- 13: /SIDS8/gcgdata/geneseq/geneseqp/AA1992.DAT.\*
- 14: /SIDS8/gcgdata/geneseq/geneseqp/AA1993.DAT.\*
- 15: /SIDS8/gcgdata/geneseq/geneseqp/AA1994.DAT.\*
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- 19: /SIDS8/gcgdata/geneseq/geneseqp/AA1998.DAT.\*
- 20: /SIDS8/gcgdata/geneseq/geneseqp/AA1999.DAT.\*
- 21: /SIDS8/gcgdata/geneseq/geneseqp/AA2000.DAT.\*
- 22: /SIDS8/gcgdata/geneseq/geneseqp/AA2001.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	96	100.0	60	21	AAV92354
2	96	100.0	61	21	AAV92352
3	96	100.0	180	21	AAV92351
4	96	100.0	280	21	AAV92355
5	96	100.0	400	21	AAV92350
6	96	100.0	401	18	AAW11156
7	96	100.0	417	10	AAV92276
8	96	100.0	417	20	AAV00927
9	96	100.0	417	21	AAV92349
10	91	94.8	403	17	AAW04171
11	82	85.4	49	21	AAV92353

12	66	58.8	336	12	AA13212	Partial sequence o
13	51	53.1	848	21	AAV88565	Human NCAM 140kd 1
14	48	50.0	17	20	AAV21879	Peptide Seq ID No:
15	48	50.0	17	20	AAV09101	Cell adhesion reco
16	48	50.0	17	21	AAV78215	N-CAM heparin bind
17	48	50.0	17	21	AAV64629	Cell adhesion reco
18	44	45.8	295	22	AAV62466	S. pombe Chk1 kina
19	44	45.8	496	22	AAE00857	Schizosaccharomyce
20	43	44.8	14	21	AAV10751	Fibrin gel binding
21	43	44.8	14	21	AAV01586	Proteoglycan bindi
22	43	44.8	14	22	AAV35931	NCAM/heparin bindi
23	43	44.8	22	21	AAV10761	Fibrin gel binding
24	43	44.8	318	20	AAV28509	Fen(Y205D) mutant
25	43	44.8	415	22	AAV66341	Castor bean calret
26	43	44.8	415	22	AAV66343	Castor bean calret
27	43	44.8	805	21	AAV28141	Sucrose synthase p
28	43	44.8	805	21	AAV16282	Eucalyptus grandis
29	43	44.8	805	21	AAV16336	Eucalyptus grandis
30	41	42.7	122	10	AAV90402	Plasmodium falcipa
31	41	42.7	198	21	AAV58162	Lung cancer associ
32	41	42.7	236	22	AAV25835	Human protein sequ
33	41	42.7	238	21	AAV21100	Human brain ring-f
34	41	42.7	250	18	AAV25144	Human (a riboso
35	41	42.7	250	18	AAV21707	Momordin. Momordi
36	41	42.7	255	22	AAV73609	Human colon cancer
37	41	42.7	263	14	AAV37296	Plant type I RIP M
38	41	42.7	263	16	AAV63908	Type I ribosome-in
39	41	42.7	263	16	AAV74182	Type I ribosome-in
40	41	42.7	355	22	AAV75504	Human colon cancer
41	41	42.7	502	12	AAV15226	HincII restriction
42	41	42.7	503	15	AAV55366	Human Activin rece
43	41	42.7	503	16	AAV5210	Human ALK-1. Homo
44	41	42.7	503	17	AAV94602	TAR-3 polypeptide.
45	41	42.7	503	18	AAV27507	Human activin rece

ALIGNMENTS

RESULT 1  
ID AAY92354 standard; Protein; 60 AA.  
XX  
AC AAY92354;  
XX  
DT 10-AUG-2000 (first entry)  
XX  
DE Recombinant human calreticulin residues 121-180.

XX MBP-calreticulin; maltose binding protein; angiogenesis; inhibition;  
KW endothelial cell; anti-angiogenic; neuroprotective; antidiabetic;  
KW cytostatic; dermalogical; immunosuppressive; antiinflammatory; hepatic;  
KW anti-atherosclerotic; gastrointestinal; anti-arthritis; ophthalmic.

OS Homo sapiens.  
OS Synthetic.

PN WO200020577-A1.

PD 13-APR-2000.

PF 05-OCT-1999; 99WO-US23240.

PR 06-OCT-1998; 98US-0103438.

PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.

PI Tosato G, Pike SE, Yao L;

XX WPI; 2000-303767/26.

DR Inhibiting endothelial cell growth and angiogenesis using calreticulin,  
XX Flea calreticulin  
PT useful for suppressing tumor growth

XX PS Claim 4; Page 85; 99pp; English.

XX CC A novel method of inhibiting endothelial cell growth comprises

CC contacting the cells with calreticulin (or its fragments/variants).

CC Fragments of calreticulin causes at least 40% inhibition of angiogenesis,

CC tumor growth and/or endothelial cell growth (claimed). The method may be

CC used for inhibiting angiogenesis in a patient. The angiogenesis is

CC associated with a disease other than a tumor that is associated with

CC neovascularization (e.g. diabetic neuropathy, retrolental fibroplasia,

CC trachoma, neovascular glaucoma, psoriasis, angiofibromas, immune

CC inflammation, atherosclerosis, excessive wound repair, retinal

CC neovascularization, macular degeneration, corneal graft rejection,

CC contact lens overwear, Crohn's disease, non-immune inflammation,

CC rheumatoid arthritis, systemic lupus erythematosus, thyroiditis,

CC Goodpasture's syndrome, systemic vasculitis, scleroderma, Sjorgen's

CC syndrome, sarcoidosis and primary biliary cirrhosis). The method may

CC also be used for treating/inhibiting tumor growth especially

XX Kaposi's sarcoma (claimed).

SQ Sequence 60 AA;

Query Match 100.0%; Score 96; DB 21; Length 60;

Best Local Similarity 100.0%; Pred. No. 1.7e-09;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VIFNYKGNVINKDIRC 18

XXXXXXXXXXXXXXXXXX

DB 9 vifnykgknvinkdirc 26

## RESULT 2

AAY92352

ID AAY92352 standard; Protein; 61 AA.

XX AC AAY92352;

XX 10-AUG-2000 (first entry)

XX Recombinant human calreticulin residues 120-180.

XX MBP-calreticulin; maltose binding protein; angiogenesis; inhibition;

KW endothelial cell; anti-angiogenic; neuroprotective; antidiabetic;

KW cytotatic; dermalogical; immunosuppressive; antiinflammatory; hepatic;

KW anti-atherosclerotic; gastrointestinal; anti-arthritis; ophthalmic.

XX OS Homo sapiens.

XX OS Synthetic.

XX WO200020577-A1.

XX 13-APR-2000.

XX 05-OCT-1999; 99WO-US23240.

XX 06-OCT-1998; 98US-0103438.

XX (USSH ) US DEPT HEALTH & HUMAN SERVICES.

XX Tosato G, Pike SE, Yao L;

XX WPI; 2000-303767/26.

XX Inhibiting endothelial cell growth and angiogenesis using calreticulin,

PT useful for suppressing tumor growth

XX Claim 4; Page 82-83; 99pp; English.

XX A novel method of inhibiting endothelial cell growth comprises

CC contacting the cells with calreticulin (or its fragments/variants).

CC Fragments of calreticulin causes at least 40% inhibition of angiogenesis,

CC tumor growth and/or endothelial cell growth (claimed). The method may be

CC used for inhibiting angiogenesis in a patient. The angiogenesis is

CC associated with a disease other than a tumor that is associated with

CC neovascularization (e.g. diabetic neuropathy, retrolental fibroplasia,

CC trachoma, neovascular glaucoma, psoriasis, angiofibromas, immune

CC inflammation, atherosclerosis, excessive wound repair, retinal

CC neovascularization, macular degeneration, corneal graft rejection,

CC contact lens overwear, Crohn's disease, non-immune inflammation,

CC rheumatoid arthritis, systemic lupus erythematosus, thyroiditis,

CC Goodpasture's syndrome, systemic vasculitis, scleroderma, Sjorgen's

CC syndrome, sarcoidosis and primary biliary cirrhosis). The method may

CC also be used for treating/inhibiting tumor growth especially

XX Kaposi's sarcoma (claimed).

SQ Sequence 61 AA;

Query Match 100.0%; Score 96; DB 21; Length 61;

Best Local Similarity 100.0%; Pred. No. 1.7e-09;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VIFNYKGNVINKDIRC 18

XXXXXXXXXXXXXXXXXX

DB 10 vifnykgknvinkdirc 27

## RESULT 3

AAY92351

ID AAY92351 standard; Protein; 180 AA.

XX AC AAY92351;

XX 10-AUG-2000 (first entry)

XX Human vasostatin (calreticulin N-terminal 180 amino acids).

XX MBP-calreticulin; maltose binding protein; vasostatin; N-terminal;

KW angiogenesis; inhibition; endothelial cell; anti-angiogenic;

KW neuroprotective; antidiabetic; cytotatic; dermalogical; hepatic;

KW immunosuppressive; antiinflammatory; anti-atherosclerotic;

KW gastrointestinal; anti-arthritis; ophthalmic.

XX OS Homo sapiens.

XX OS Synthetic.

XX WO200020577-A1.

XX 13-APR-2000.

XX 05-OCT-1999; 99WO-US23240.

XX 06-OCT-1998; 98US-0103438.

XX (USSH ) US DEPT HEALTH & HUMAN SERVICES.

XX Tosato G, Pike SE, Yao L;

XX WPI; 2000-303767/26.

XX Inhibiting endothelial cell growth and angiogenesis using calreticulin,

PT useful for suppressing tumor growth

XX Claim 4; Page 82; 99pp; English.

XX A novel method of inhibiting endothelial cell growth comprises

CC contacting the cells with calreticulin (or its fragments/variants).

CC Fragments of calreticulin causes at least 40% inhibition of angiogenesis,

CC tumor growth and/or endothelial cell growth (claimed). The method may be

CC used for inhibiting angiogenesis in a patient. The angiogenesis is

CC associated with a disease other than a tumor that is associated with

CC neovascularization (e.g. diabetic neuropathy, retrolental fibroplasia,

CC trachoma, neovascular glaucoma, psoriasis, angiofibromas, immune

CC inflammation, atherosclerosis, excessive wound repair, retinal

CC neovascularization, macular degeneration, corneal graft rejection,

CC contact lens overwear, Crohn's disease, non-immune inflammation,  
 CC rheumatoid arthritis, systemic lupus erythematosus, thyroiditis,  
 CC Goodpasture's syndrome, systemic vasculitis, scleroderma, Sjorgen's  
 CC syndrome, sarcoidosis and primary biliary cirrhosis). The method may  
 CC also be used for treating/inhibiting tumor growth especially  
 CC Kaposi's sarcoma (claimed).  
 XX  
 SQ Sequence 180 AA;

Query Match 100.0%; Score 96; DB 21; Length 180;  
 Best Local Similarity 100.0%; Pred. No. 6.4e-09;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VIFNYGKNVLINKDIRC 18  
 Db 129 vifnygknvlinkdirc 146  
 |||||

RESULT 4  
 AAY92355  
 ID AAY92355 standard; Protein: 280 AA.  
 XX  
 AC AAY92355;  
 XX  
 DT 10-AUG-2000 (first entry)  
 XX  
 DE Recombinant delta-120 calreticulin.  
 XX  
 KW MBP-calreticulin; maltose binding protein; angiogenesis; inhibition;  
 KW endothelial cell; anti-angiogenic; neuroprotective; antidiabetic;  
 KW cytostatic; dermatological; immunosuppressive; antiinflammatory; hepatic;  
 KW anti-atherosclerotic; gastrointestinal; anti-arthritis; ophthalmic.  
 XX  
 OS Homo sapiens.  
 OS Synthetic.  
 XX  
 PN WO200020577-A1.  
 XX  
 PD 13-APR-2000.  
 XX  
 PF 05-OCT-1999; 99WO-US23240.  
 XX  
 PR 06-OCT-1998; 98US-0103438.  
 XX  
 PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.  
 XX  
 PI Tosato G, Pike SE, Yao L;  
 XX  
 PS WPI; 2000-303767/26.  
 XX  
 PT Inhibiting endothelial cell growth and angiogenesis using calreticulin,  
 PT useful for suppressing tumor growth  
 XX  
 PS Claim 4; Page 86; 99pp; English.  
 XX  
 CC This sequence comprises recombinant human calreticulin (AAY92355)  
 CC missing the N-terminal 120 amino acids.  
 CC A novel method of inhibiting endothelial cell growth comprises  
 CC contacting the cells with calreticulin (or its fragments/variants).  
 CC Fragments of calreticulin causes at least 40% inhibition of  
 CC angiogenesis, tumor growth and/or endothelial cell growth (claimed). The  
 CC method may be used for inhibiting angiogenesis in a patient. The  
 CC angiogenesis is associated with a disease other than a tumor that is  
 CC associated with neovascularization (e.g. diabetic neuropathy, retrolental  
 CC fibroplasia, trachoma, neovascular glaucoma, psoriasis, angiofibromas,  
 CC immune inflammation, atherosclerosis, excessive wound repair, retinal  
 CC neovascularization, macular degeneration, corneal graft rejection,  
 CC contact lens overwear, Crohn's disease, non-immune inflammation,  
 CC rheumatoid arthritis, systemic lupus erythematosus, thyroiditis,  
 CC Goodpasture's syndrome, systemic vasculitis, scleroderma, Sjorgen's  
 CC syndrome, sarcoidosis and primary biliary cirrhosis). The method may  
 CC also be used for treating/inhibiting tumor growth especially

CC Kaposi's sarcoma (claimed).  
 XX  
 SQ Sequence 280 AA;

Query Match 100.0%; Score 96; DB 21; Length 280;  
 Best Local Similarity 100.0%; Pred. No. 1.1e-08;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VIFNYGKNVLINKDIRC 18  
 Db 9 vifnygknvlinkdirc 26  
 |||||

RESULT 5  
 AAY92350  
 ID AAY92350 standard; Protein: 400 AA.  
 XX  
 AC AAY92350;  
 XX  
 DT 10-AUG-2000 (first entry)  
 XX  
 DE Recombinant human MBP-calreticulin.  
 XX  
 KW MBP-calreticulin; maltose binding protein; angiogenesis; inhibition;  
 KW endothelial cell; anti-angiogenic; neuroprotective; antidiabetic;  
 KW cytostatic; dermatological; immunosuppressive; antiinflammatory; hepatic;  
 KW anti-atherosclerotic; gastrointestinal; anti-arthritis; ophthalmic.  
 XX  
 OS Homo sapiens.  
 OS WO200020577-A1.  
 PN  
 PD 13-APR-2000.  
 XX  
 PF 05-OCT-1999; 99WO-US23240.  
 XX  
 PR 06-OCT-1998; 98US-0103438.  
 XX  
 PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.  
 XX  
 PI Tosato G, Pike SE, Yao L;  
 XX  
 DR WPI; 2000-303767/26.  
 DR N-PSDB; AAA09346, AAA09347.  
 XX  
 PT Inhibiting endothelial cell growth and angiogenesis using calreticulin,  
 PT useful for suppressing tumor growth  
 XX  
 PS Claim 4; Page 80-81; 99pp; English.  
 XX  
 CC Recombinant human MBP-calreticulin comprises the sequence of human  
 CC calreticulin (see AAY92349) without the 17 N-terminal amino acids.  
 CC A novel method of inhibiting endothelial cell growth comprises  
 CC contacting the cells with calreticulin (or its fragments/variants).  
 CC Fragments of calreticulin causes at least 40% inhibition of  
 CC angiogenesis, tumor growth and/or endothelial cell growth (claimed). The  
 CC method may be used for inhibiting angiogenesis in a patient. The  
 CC angiogenesis is associated with a disease other than a tumor that is  
 CC associated with neovascularization (e.g. diabetic neuropathy, retrolental  
 CC fibroplasia, trachoma, neovascular glaucoma, psoriasis, angiofibromas,  
 CC immune inflammation, atherosclerosis, excessive wound repair, retinal  
 CC neovascularization, macular degeneration, corneal graft rejection,  
 CC contact lens overwear, Crohn's disease, non-immune inflammation,  
 CC rheumatoid arthritis, systemic lupus erythematosus, thyroiditis,  
 CC Goodpasture's syndrome, systemic vasculitis, scleroderma, Sjorgen's  
 CC syndrome, sarcoidosis and primary biliary cirrhosis). The method may  
 CC also be used for treating/inhibiting tumor growth especially  
 CC Kaposi's sarcoma (claimed).  
 XX  
 SQ Sequence 400 AA;

Query Match 100.0%; Score 96; DB 21; Length 400;  
 Best Local Similarity 100.0%; Pred. No. 1.7e-08;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VIFNYKGNVLINKDIRC 18  
 |||||  
 DB 129 VIFNYKGNVLINKDIRC 146

## RESULT 6

AAW11156  
 ID AAW11156 standard; peptide; 401 AA.

AC AAW11156;

DT 31-MAY-1997 (first entry)

DE Calreticulin.

KW calreticulin; C-domain; restenosis; inhibitor.

OS Homo sapiens.

PN WO967643-A1.

PD 21-NOV-1996.

PF 17-MAY-1996; 96WO-1B00471.

PR 16-MAY-1996; 96US-0649417.

PR 17-MAY-1995; 95US-0442844.

PA (UYAL-) UNIV ALBERTA.

PI LARSEN A, Michalak M;

XX WPI; 1997-012036/01.

XX Inhibition of restenosis in patients - using calreticulin or a  
 PT C-domain polypeptide of calreticulin or a variant with the same  
 PT activity.

XX Disclosure; Fig 1; 48pp; English.

XX The present sequence is calreticulin. It and a C-domain derived peptide  
 CC (AAW06736) are useful for treating a patient to inhibit restenosis. The  
 CC calreticulin-type cpds. are administered either parenterally,  
 CC intravenously or via a catheter and can target areas of vascular damage  
 CC to inhibit or prevent restenosis.

XX Sequence 401 AA;

Query Match 100.0%; Score 96; DB 18; Length 401;  
 Best Local Similarity 100.0%; Pred. No. 1.7e-08;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VIFNYKGNVLINKDIRC 18  
 |||||  
 DB 129 VIFNYKGNVLINKDIRC 146

## RESULT 7

AAP92276  
 ID AAP92276 standard; protein; 417 AA.

XX AAP92276;

DT 23-FEB-1990 (first entry)

XX 60 kD Ro (Ro/SSA) antigen.

XX Sjogren's syndrome; systemic lupus erythematosus.

XX Synthetic.  
 OS WO8909273-A.  
 PN 05-OCT-1989.  
 PD 22-MAR-1989; 89WO-US01213.  
 PF 22-MAR-1988; 88US-0171634.  
 PR (TEXA ) UNIV OF TEXAS SYST.  
 PA Sontheimer RD, Capra JD, McCauliffe DP;  
 PI WPI; 1989-309537/42.  
 XX N-PSDB; AAP92276.  
 DR DNA sequences encoding antigenic epitope(s) of Ro 60 kD autoantigen  
 PT - used in immunoassays to detect rheumatic disease  
 XX Disclosure; Fig 2; 88pp; English.  
 XX Synthetic peptides corresp. to an epitopic core of Ro antigen are  
 CC expressed recombinantly to detect autoantibodies, for identification  
 CC of autoimmune diseases. These epitopes are AAs 24-36, 23-36, 188-209,  
 CC or 241-255. The peptides may be substd. for ribonucleoprotein particle  
 CC antigens.  
 XX Sequence 417 AA;

Query Match 100.0%; Score 96; DB 10; Length 417;  
 Best Local Similarity 100.0%; Pred. No. 1.8e-08;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VIFNYKGNVLINKDIRC 18

DB 146 VIFNYKGNVLINKDIRC 163

## RESULT 8

AAV00927

ID AAV00927 standard; Protein; 417 AA.

XX AAV00927;

XX 28-MAY-1999 (first entry)

DE Calreticulin.

XX Clq and collectin receptor; cC1qR binding domain; complement ubiquitin;  
 KW CUB functionality; inhibitor; complement activation; inflammation;  
 KW myocardial infarction; brain ischaemia; gut ischaemia; amyloid plaque;  
 KW rheumatoid arthritis; systemic lupus erythematosus; Alzheimer's disease;  
 KW immune complex nephritis; therapy.

XX Homo sapiens.

PN WO9507406-A1.

PD 18-FEB-1999.

PF 12-AUG-1998; 98WO-GB02430.

PR 12-AUG-1997; 97GB-0016998.

PA (UYLE-) UNIV LEICESTER.

XX Schwaeble W;

XX WPI; 1999-180404/15.



PT Use of a cClqR binding domain - to modulate complement ubiquitin  
 PT (CUB) functionality.

XX  
 PS Disclosure: Page 26-27; 31pp; English.

XX This sequence is calreticulin, a homologue of Clq and collectin receptor  
 CC (cClqR). The invention relates to the use of a cClqR binding domain in a  
 CC medicament to effect complement ubiquitin (CUB) functionality, and an  
 CC inhibitor of the cClqR binding domain in a medicament to inhibit CUB  
 CC functionality. The cClqR binding domain, or its inhibitor, can be used to  
 CC treat a human or animal body. Particularly an inhibitor is used to treat  
 CC complement activation involved in the initiation and maintenance of  
 CC inflammation, for example in myocardial infarction, brain ischaemia  
 CC (stroke), gut ischaemia, rheumatoid arthritis, systemic lupus  
 CC erythematosus, burns, immune complex nephritis, and to treat amyloid  
 CC plaques in Alzheimer's disease. The use of cClqR binding domain or  
 CC inhibitor enables the CUB domain functionality to be modulated using a  
 CC low molecular weight molecule.

XX Sequence 417 AA;

Query Match 100.0%; Score 96; DB 20; Length 417;  
 Best Local Similarity 100.0%; Pred. No. 1.8e-08;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 VIFNYKGNVLINKDIRC 18  
 ||||||||||||||||  
 Db 146 vifnykgnvlinkdirc 163

RESULT 9

AAAY92349  
 ID AAY92349 standard; Protein; 417 AA.

XX  
 AC AAY92349;

XX 10-AUG-2000 (first entry)

XX Human MBP-calreticulin.

XX MBP-calreticulin; maltose binding protein; angiogenesis; inhibition;  
 KW endothelial cell; anti-angiogenic; neuroprotective; antidiabetic;  
 KW cytosolic; dermalogical; immunosuppressive; antiinflammatory; hepatic;  
 KW anti-atherosclerotic; gastrointestinal; anti-arthritis; ophthalmic.

XX Homo sapiens.

XX Key Location/Qualifiers  
 FH Peptide 1..17  
 FT /label= signal\_peptide  
 FT Protein 18  
 FT /label= mature\_protein

XX WO200020577-A1.

XX 13-APR-2000.

XX 05-OCT-1999; 99WO-US23240.

XX 06-OCT-1998; 98US-0103438.

XX (USSH ) US DEPT HEALTH & HUMAN SERVICES.

XX Tosato G, Pike SE, Yao L;

XX WPI; 2000-303767/26.

DR N-PSDB; AAA09346, AAA09347.

XX Inhibiting endothelial cell growth and angiogenesis using calreticulin,  
 PT useful for suppressing tumor growth

XX Disclosure: Page 79-80; 99pp; English.

XX A novel method of inhibiting endothelial cell growth comprises  
 CC contacting the cells with calreticulin (or its fragments/variants).  
 CC Fragments of calreticulin causes at least 40% inhibition of angiogenesis.  
 CC tumor growth and/or endothelial cell growth (claimed). The method may be  
 CC used for inhibiting angiogenesis in a patient. The angiogenesis is  
 CC associated with a disease other than a tumor that is associated with  
 CC neovascularization (e.g. diabetic neuropathy, retrolental fibroplasia,  
 CC trachoma, neovascular glaucoma, psoriasis, angiofibromas, immune  
 CC inflammation, atherosclerosis, excessive wound repair, retinal  
 CC neovascularization, macular degeneration, corneal graft rejection,  
 CC contact lens overwear, Crohn's disease, non-immune inflammation,  
 CC rheumatoid arthritis, systemic lupus erythematosus, thyroiditis,  
 CC Gompasture's syndrome, systemic vasculitis, scleroderma, Sjorgen's  
 CC syndrome, sarcoidosis and primary biliary cirrhosis). The method may  
 CC also be used for treating/inhibiting tumor growth especially  
 CC Kaposi's sarcoma (claimed).

XX Sequence 417 AA;

Query Match 100.0%; Score 96; DB 21; Length 417;  
 Best Local Similarity 100.0%; Pred. No. 1.8e-08;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 VIFNYKGNVLINKDIRC 18  
 ||||||||||||||||  
 Db 146 vifnykgnvlinkdirc 163

RESULT 10

AAW04171

ID AAW04171 standard; Protein; 403 AA.

XX  
 AC AAW04171;

XX 12-DEC-1996 (first entry)

XX Flea calreticulin PctCal403.

XX Calreticulin; flea; haematophagous insect; allergic dermatitis;  
 KW vaccine; therapy; PctCal403.

XX Ctenocephalides felis.

XX WO9628469-A1.

XX 19-SEP-1996.

XX 08-MAR-1996; 96WO-US03133.

XX 09-MAR-1995; 95US-0401509.

XX (HESK-) HESKA CORP.

XX Rushlow KE, Stiegler GL;

XX WPI; 1996-442861/44.

XX N-PSDB; AAT39516;

XX N-PSDB; AAT39517.

XX Haematophagous insect calreticulin protein - used to reduce insect

XX infestation and desensitise patients to allergic dermatitis

XX Claim 5; Page 68-69; 86pp; English.

XX Flea calreticulin protein PctCall1589 (AAW04171) is a calcium-binding

CC protein found in the salivary glands of Ctenocephalides felis.

CC Its amino acid sequence was deduced from a cDNA clone (AAT39516)

CC obtd. from a salivary gland cDNA library. Recombinant PctCall1589

CC can be produced in host cells transformed with a vector carrying

CC calreticulin nucleic acids. Calreticulin alters the blood feeding

CC behaviour of haematophagous insects and can be administered to an

CC animal to reduce infestation. It reduces calreticulin activity in  
 CC insects, so reducing the insect burden on an animal. Calreticulin  
 CC can be used to elicit an immune response, thereby desensitising an  
 CC animal to allergic dermatitis caused by fleas, mosquitoes or  
 CC Culicoides.

XX SQ Sequence 403 AA;

Query Match 94.8%; Score 91; DB 17; Length 403;

Best Local Similarity 94.4%; Pred. No. 1.2e-07;

Matches 17; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 VIFNYKGNVLINKDIRC 18

DB 146 VIFS YKGNVLINKDIRC 163

RESULT 11

AA92353

ID AAY92353 standard; Protein; 49 AA.

XX AC AAY92353;

XX DT 10-AUG-2000 (first entry)

XX DE Recombinant human calreticulin residues 132-180.

XX KW MRP-calreticulin; maltose binding protein; angiogenesis; inhibition;  
 KW endothelial cell; anti-angiogenic; neuroprotective; antidiabetic;  
 KW cytostatic; dermatologic; immunosuppressive; antiinflammatory; hepatic;  
 KW anti-atherosclerotic; gastrointestinal; anti-arthritis; ophthalmic.

XX OS Homo sapiens.

XX SN Synthetic.

XX PN WO200020577-A1.

XX PD 13-APR-2000.

XX PF 05-OCT-1999; 99WO-US23240.

XX PR 06-OCT-1998; 98US-0103438.

XX PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.

XX PI Toshato G, Pike SE, Yao L;

XX WPI; 2000-303767/26.

XX PT Inhibiting endothelial cell growth and angiogenesis using calreticulin,  
 PT useful for suppressing tumor growth

XX PS Claim 4; Page 82-83; 99pp; English.

XX CC A novel method of inhibiting endothelial cell growth comprises  
 CC contacting the cells with calreticulin (or its fragments/variants).  
 CC Fragments of calreticulin causes at least 40% inhibition of angiogenesis,  
 CC tumor growth and/or endothelial cell growth (claimed). The method may be  
 CC used for inhibiting angiogenesis in a patient. The angiogenesis is  
 CC associated with a disease other than a tumor that is associated with  
 CC neovascularization (e.g. diabetic neuropathy, retrolental fibroplasia,  
 CC trachoma, neovascular glaucoma, psoriasis, angiofibromas, immune  
 CC inflammation, atherosclerosis, excessive wound repair, retinal  
 CC neovascularization, macular degeneration, corneal graft rejection,  
 CC contact lens overwear, Crohn's disease, non-immune inflammation,  
 CC rheumatoid arthritis, systemic lupus erythematosus, thyroiditis,  
 CC Goodpasture's syndrome, systemic vasculitis, scleroderma, Sjorgen's  
 CC syndrome, sarcoidosis and primary biliary cirrhosis). The method may  
 CC also be used for treating/inhibiting tumor growth especially  
 CC Kaposi's sarcoma (claimed).

XX SQ Sequence 49 AA;

Query Match 85.4%; Score 82; DB 21; Length 49;  
 Best Local Similarity 100.0%; Pred. No. 3.7e-07;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 NYKGNVLINKDIRC 18

DB 1 nykgknvlinkdirc 15

RESULT 12

AA912312

ID AAR12312 standard; Protein; 336 AA.

XX AC AAR12312;

XX DT 29-AUG-1991 (first entry)

XX DE Partial sequence of Onchocera volvulus 42 kD antigen.

XX KW River blindness; onchocerciasis; vaccine; antigen; parasite.

XX OS Onchocerca volvulus.

XX FH Key Location/Qualifiers  
 XX Region 160..166  
 XX /label= repeat unit  
 XX /note= "hydrophilic"

XX FT Region 177..183  
 XX /label= repeat unit  
 XX /note= "hydrophilic"

XX FT Region 195..201  
 XX /label= repeat unit  
 XX /note= "hydrophilic"

XX FT US5021342-A.

XX PD 04-JUN-1991.

XX PF 30-JUN-1988; 88US-0214264.

XX PR 30-JUN-1988; 88US-0214264.

XX PA (UYHO-) UNIV HOSPITALS CLEV.

XX PI Greene BM, Unnasch TR;

XX WPI; 1991-185179/25.

XX DR N-PSDB; AAQ11987.

XX PT DNA encoding Onchocerca volvulus antigen - used to express  
 PT recombinant antigen for vaccine against onchocerciasis or river  
 PT blindness.

XX PS Disclosure; Fig 7; 20pp; English.

XX CC The sequence was deduced from a cDNA clone lambda RAL-1 prepd.  
 CC from RNA isolated from nodules excised from patients infected  
 CC with O. volvulus. The N-terminal is incomplete, however Abs  
 CC which specifically bind to protein prepd. from induced cultures  
 CC of lambda RAL-1 lysogens recognise a single polypeptide of mol.  
 CC wt. 42,000 in extracts of adult worms. Analysis deduced sequence  
 CC suggests that it encodes a protein of mol. wt. 39,130. If the  
 CC antigen is not subject to post-translational processing this  
 CC suggests that most of the coding sequence is present. The three  
 CC repeats are highly hydrophilic regions likely to be exposed on  
 CC the surface of the antigen and highly immunogenic. Recombinant  
 CC antigen expressed by the clone can be used stimulate T-cells of  
 CC individuals infected by the parasite to proliferate and may be  
 CC used as the basis for a vaccine against Onchocerciasis or river  
 CC blindness.

XX

SQ Sequence 336 AA; Query Match 68.8%; Score 66; DB 12; Length 336; Best Local Similarity 66.7%; Pred. No. 0.0023; Matches 12; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 VIFNYKGNVLINKDIR 18  
||||| :| :| |||||

Db 92 vifhykdrnhmikkdir 109

RESULT 13  
AAV88565  
ID AAV88565 standard; protein; 848 AA.  
AC AAV88565;  
XX  
XX  
DT 07-AUG-2000 (first entry)  
XX  
XX  
DE Human NCAM 140kD isoform precursor amino acid sequence.  
XX  
KW NCAM; neural cell adhesion molecule; Ig1; immunoglobulin domain 1;  
KW neurite outgrowth promoter; proliferation; nerve damage; sclerosis;  
KW impaired myelination; stroke; Parkinson's disease; memory; schizophrenia;  
KW Alzheimer's disease; diabetes mellitus; circadian clock; nephrosis;  
KW treatment; prosthetic nerve guide; treatment; nervous system.  
XX  
OS Homo sapiens.  
XX  
XX  
PN WO200018801-A2.  
XX  
XX  
PD 06-APR-2000.  
XX  
XX  
PF 23-SEP-1999; 99WO-DK00500.  
XX  
XX  
PR 29-SEP-1998; 98DK-0001232.  
PR 29-APR-1999; 99DK-0000592.  
XX  
XX  
PA (RONN/) RONN L C B.  
PA (BOCK/) BOCK E.  
PA (HOLM/) HOLM A.  
PA (OLSE/) OLSEN M.  
PA (OSTE/) OSTERGAARD S.  
PA (JENS/) JENSEN P H.  
PA (POUL/) POULSEN F M.  
PA (SORO/) SOROKA V.  
PA (RALE/) RALETS I.  
PA (BERE/) BEREZIN V.  
XX  
XX  
PI Ronn LCB, Bock E, Holm A, Olsen M, Ostergaard S, Jensen PH;  
PI Poulsen FM, Soroka V, Ralets I, Berezin V;  
XX  
XX  
DR WPI: 2000-293111/25.  
XX  
XX  
PT Compositions that bind neural cell adhesion molecules useful for  
PT treating disorders of the nervous system and muscles e.g. Alzheimer's  
PT and Parkinson's diseases -  
XX  
XX  
PS Disclosure: Fig 17; 119pp; English.  
XX  
XX  
CC This sequence represents the human neural cell adhesion molecule (NCAM)  
CC amino acid sequence. NCAM is found in three forms, two of which are  
CC transmembrane forms, while the third is attached via a lipid anchor to  
CC the cell membrane. All three NCAM forms have an extracellular structure  
CC consisting of five immunoglobulin domains (Ig domains). The Ig domains are  
CC numbered 1 to 5 from the N-terminal. The invention relates to a compound  
CC containing a peptide which binds to the NCAM Ig1 domain. The compound  
CC binds to NCAM-Ig1/Ig2 domains, and is capable of stimulating or promoting  
CC neurite outgrowth from NCAM presenting cells, and is also capable of  
CC promoting the proliferation of NCAM presenting cells. The compound may be  
CC used in the treatment of normal, degenerated or damaged NCAM presenting  
CC cells. The compound may in particular be used to treat diseases of the

CC central and peripheral nervous systems such as post operative nerve  
CC damage, traumatic nerve damage, impaired myelination of nerve fibres,  
CC conditions resulting from a stroke, Parkinson's disease, Alzheimer's  
CC disease, dementias, sclerosis, nerve degeneration associated with  
CC diabetes mellitus, disorders affecting the circadian clock or  
CC neuro-muscular transmission and schizophrenia. Conditions affecting the  
CC muscles may also be treated with the compound, such as conditions  
CC associated with impaired function of neuromuscular connections  
CC (e.g. genetic or traumatic shock or traumatic atrophic muscle disorders).  
CC Conditions of the gonads, pancreas (e.g. diabetes mellitus types I and  
CC II), kidney (e.g. nephrosis), heart, liver and bowel may also be treated  
CC using the compound. The compound is used in a prosthetic nerve guide, and  
CC also to stimulate the ability to learn, and to stimulate the memory of a  
CC subject.  
XX  
XX  
SQ Sequence 848 AA;

Query Match 53.1%; Score 51; DB 21; Length 848;  
Best Local Similarity 41.2%; Pred. No. 2.9;  
Matches 7; Conservative 8; Mismatches 2; Indels 0; Gaps 0;

QY 1 VIFNYKGNVLINKDIR 17  
:| :| :| :| :| :| :| :|

Db 149 ilwkhgrdvilkdv 165

RESULT 14  
AAV21879  
ID AAV21879 standard; peptide; 17 AA.  
XX  
XX  
AC AAV21879;  
XX  
XX  
DT 20-SEP-1999 (first entry)  
XX  
XX  
DE Peptide Seq ID No: 63 of WO9933875.  
XX  
KW Cell adhesion modulation; CAM; synaptic stability; cadherin;  
KW cadherin-mediated adhesion; drug delivery; cell adhesion; tumour;  
KW wound healing; neurite outgrowth.  
XX  
XX  
OS Synthetic.  
XX  
XX  
PN WO9933875-A1.  
XX  
XX  
PD 08-JUL-1999.  
XX  
XX  
PF 23-DEC-1998; 98WO-CA01207.  
XX  
XX  
PR 23-DEC-1997; 97US-0996679.  
XX  
XX  
PA (UYMC-) UNIV MCGILL.  
XX  
XX  
PI Blaschuk OW, Gour BJ;  
XX  
XX  
DR WPI: 1999-430231/36.  
XX  
XX  
PT Cyclic peptide cell adhesion modulating agents, useful for  
PT modulating synaptic stability  
XX  
XX  
PS Examples; Page 139; 144pp; English.  
XX  
XX  
CC The invention provides cyclic peptide cell adhesion modulating (CAM)  
CC agents that comprises a His-Ala-Val recognition sequence. Also provided  
CC is a method for inhibiting synaptic stability in a mammal that comprises  
CC administering to a mammal a therapeutically effective amount of a CAM  
CC agent that inhibits cadherin-mediated adhesion, where the agent comprises  
CC a cyclic peptide having a peptide ring, and where the sequence His-Ala-  
CC Val is present within the peptide ring. The cyclic peptides are cell  
CC adhesion modulating agents that inhibit cadherin-mediated adhesion. They  
CC can be used in a method for inhibiting synaptic stability in mammals. The  
CC agents can be used to treat diseases or other conditions characterized by  
CC undesirable cell adhesion or to facilitate drug delivery to a specific

CC tissue or tumour. Alternatively the agents may be used to enhance cell  
CC adhesion (e.g. to supplement or replace stitches or to facilitate wound  
CC healing) or to enhance or direct neurite outgrowth.

XX SQ Sequence 17 AA;

Query Match 50.0%; Score 48; DB 20; Length 17;  
Best Local Similarity 43.8%; Pred. No. 0.087;  
Matches 7; Conservative 7; Mismatches 2; Indels 0; Gaps 0;

QY 2 IFNYKGNVLLINKDIR 17  
Db 1 lwkhgrdvllkkdvr 16  
| : : : : : | : : |  
| : : : : : | : : |

RESULT 15  
AAY09101  
ID AAY09101 standard; peptide; 17 AA.

XX AC AAY09101;

XX DT 07-JUL-1999 (first entry)

XX DE Cell adhesion recognition (CAR) sequence.

XX KW Cadherin; modulating agent; cadherin-mediated cell adhesion; cancer;  
KW drug delivery; bladder tumour; ovarian tumour; melanoma; cell adhesion;  
KW wound healing; neurite outgrowth; demyelinating neurological disease;  
KW multiple sclerosis; carcinoma; leukemia; melanoma; angiogenesis; CAR;  
KW apoptosis; diabetes; rheumatoid arthritis; immune system; pregnancy;  
KW vasopermeability; spinal cord injury; synaptic stability.

XX OS Synthetic.

XX PN WC9916791-A2.

XX PD 08-APR-1999.

XX PF 29-SEP-1998; 98WO-CA00902.

XX PR 29-SEP-1997; 97US-0939853.

XX PA (ADHE-) ADHEREX INC.

XX PI Blaschuck OW, Gour BJ;

XX PS WPI; 1999-263686/22.

XX DR Modulating cadherin-mediated cell adhesion useful for treating  
XX PT neurological disease and cancer

XX PS Disclosure; Page 34; 148pp; English.

XX CC The invention relates to methods using cadherin modulating agents,  
XX particularly peptides containing the sequence HAV or antibodies, for  
XX enhancing or inhibiting cadherin-mediated cell adhesion. The methods  
XX can be used to treat diseases or other conditions characterized by  
XX undesirable cell adhesion or to facilitate drug delivery to a specific  
XX tissue or tumour (such as bladder tumours, ovarian tumours or melanomas).  
XX They can also be used to enhance cell adhesion (e.g. supplement or  
XX replace stitches or to facilitate wound healing). They can also be used  
XX for enhancing and/or directing neurite outgrowth. The methods can also be  
XX used for treating demyelinating neurological disease, e.g. multiple  
XX sclerosis. The methods can also be used for e.g. enhancing drug delivery,  
XX treating cancers (such as carcinomas, leukemia or melanomas), inhibiting  
XX angiogenesis, enhancing adhesion of foreign tissue implanted in a mammal,  
XX inducing apoptosis in cadherin-expressing cells, e.g. for treating  
XX diabetes or rheumatoid arthritis, modulating the immune system, for  
XX preventing pregnancy, increasing vasopermeability, treating spinal cord  
XX injuries or inhibiting synaptic stability.

XX SQ Sequence 17 AA;

Query Match 50.0%; Score 48; DB 20; Length 17;  
Best Local Similarity 43.8%; Pred. No. 0.087;  
Matches 7; Conservative 7; Mismatches 2; Indels 0; Gaps 0;

QY 2 IFNYKGNVLLINKDIR 17  
Db 1 lwkhgrdvllkkdvr 16  
| : : : : : | : : |  
| : : : : : | : : |

Search completed: January 9, 2002, 15:01:13  
Job time: 159 sec

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OM protein - protein search, using sw model

Run on: January 9, 2002, 15:01:18 ; Search time 25.18 Seconds  
(without alignments)  
262.100 Million cell updates/sec

Title: US-09-828-000-3  
Perfect score: 971  
Sequence: 1 EPAVYFKEQFLDGDGWTSM.....PONTYEVKIDNSQVESGSLE 180

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 100059 seqs, 36664827 residues

Total number of hits satisfying chosen parameters: 100059

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SwissProt\_39.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	971	100.0	417	1	CRTC_HUMAN
2	933	96.1	416	1	CRTC_RAT
3	931	95.9	418	1	CRTC_RABIT
4	930	95.8	400	1	CRTL_BOVIN
5	930	95.8	416	1	CRTC_MOUSE
6	699	72.0	406	1	CRTC_DROME
7	664	68.4	388	1	RALI_ONCVO
8	619.5	63.8	395	1	CRTC_CABEL
9	537	55.3	424	1	CRTC_DICDI
10	535.5	55.1	401	1	CRTC_EUGGR
11	531	54.7	416	1	CRTC_BETVU
12	527	54.3	415	1	CRTC_RICCO
13	527	54.3	421	1	CRTC_PRUAR
14	527	54.3	424	1	CRTC_ORISA
15	522.5	53.8	421	1	CRTL_BOVIN
16	522	53.8	416	1	CRTC_NICPL
17	518	53.3	424	1	CRTL_ARATH
18	512	52.7	420	1	CRTC_CHLRE
19	512	52.7	425	1	CRTL_ARATH
20	509	52.4	416	1	CRTC_BERST
21	504	51.9	393	1	CRTC_SCHMA
22	494	50.9	420	1	CRTC_MAIZE
23	455.5	46.9	424	1	CRTL_ARATH
24	447	46.0	105	1	CRTC_PIG
25	293	30.2	591	1	CALX_MOUSE
26	290	29.9	591	1	CALX_RAT
27	290	29.9	593	1	CALX_CANFA
28	288	29.7	592	1	CALX_HUMAN
29	270	27.8	611	1	CALG_MOUSE
30	261	26.9	610	1	CALG_HUMAN
31	253.5	26.1	560	1	CALX_SCHPO
32	244	25.1	619	1	CALX_CABEL
33	238.5	24.6	530	1	CAX1_ARATH

34	232	23.9	546	1	CALX_SOYBN
35	215.5	22.2	540	1	CALX_HELTU
36	215.5	22.2	551	1	CALX_PEA
37	202.5	20.9	528	1	CAX2_ARATH
38	133.5	13.7	502	1	CALX_YEAST
39	86	8.9	24	1	CRTC_CANFA
40	81	8.3	410	1	EFU_MESVI
41	80.5	8.3	540	1	MTAL_ACICA
42	79.5	8.2	510	1	PROI_LISMO
43	78.5	8.1	344	1	ABIC_LACIA
44	78	8.0	928	1	HXA2_HAEIN
45	77.5	8.0	659	1	AMIA_STRPN

Q39817 glycine max  
Q39994 helianthus  
O82709 pisum sativ  
Q35798 arabidopsis  
P27825 saccharomyc  
P28490 canis famli  
Q9mup0 mesostigma  
P25201 acinetobact  
P23224 listeria mo  
O01457 lactococcus  
P45354 haemophilus  
P18791 streptococc

#### ALIGNMENTS

RESULT 1	
CRTC_HUMAN	
ID CRTC_HUMAN	STANDARD; PRT; 417 AA.
AC P27797;	
DT 01-AUG-1992 (Rel. 23, Created)	
DT 01-AUG-1992 (Rel. 23, Last sequence update)	
DT 20-AUG-2001 (Rel. 40, Last annotation update)	
DE CALRETICULIN PRECURSOR (CRP55) (CALREGULIN) (HACBP) (ERP60) (52 KDA	
DE RIBONUCLEOPROTEIN AUTOANTIGEN RO/SS-A).	
GN CALR OR CRTC.	
OS Homo sapiens (Human).	
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.	
OX NCBI_TaxID=9606;	
RN [1]	
RP SEQUENCE FROM N.A.	
RP MEDLINE=92013129; PubMed=1919005;	
RA Rokeach L.A., Haselby J.A., Meilof J.F., Smeenk R.J., Unnasch T.R.,	
RA Greene B.M., Hoch S.O.;	
RT "Characterization of the autoantigen calreticulin.";	
RL J. Immunol. 147:3031-3039(1991).	
RN [2]	
RP SEQUENCE FROM N.A.	
RP MEDLINE=90237213; PubMed=2332496;	
RA McCauliffe D.P., Lux F.A., Lieu T.S., Sanz I., Hanke J., Newkirk M.M.,	
RA Bachinski L.L., Itoh Y., Siciliano M.J., Reichlin M., Sontheimer R.D.,	
Capra J.D.;	
RT "Molecular cloning, expression, and chromosome 19 localization of a	
RT human Ro/SS-A autoantigen".	
RL J. Clin. Invest. 85:1379-1391(1990).	
RN [3]	
RP SEQUENCE FROM N.A.	
RP MEDLINE=92129342; PubMed=1733953;	
RA McCauliffe D.P., Yang Y.S., Wilson J., Sontheimer R.D., Capra J.D.;	
RT "The 5'-flanking region of the human calreticulin gene shares	
RT homology with the human GRP78, GRP94, and protein disulfide isomerase	
RT promoters.";	
RL J. Biol. Chem. 267:2557-2562(1992).	
RN [4]	
RP SEQUENCE FROM N.A.	
RA Lamerdin J., McCreedy P., Stillwagen S., Ramirez M., Carrano A.;	
RL Submitted (MAR-1997) to the EMBL/GenBank/DBJ databases.	
RN [5]	
RP SEQUENCE OF 18-36.	
RP MEDLINE=92002034; PubMed=1911778;	
RA Rojiani M.V., Finlay B.B., Gray V., Dedhar S.;	
RT "In vitro interaction of a polypeptide homologous to human Ro/SS-A	
RT antigen (calreticulin) with a highly conserved amino acid sequence in	
RT the cytoplasmic domain of integrin alpha subunits.";	
RL Biochemistry 30:9859-9866(1991).	
RN [6]	
RP SEQUENCE OF 18-32.	
RP MEDLINE=90380058; PubMed=2400400;	
RA Krause K.H., Simmerman H.K.B., Jones L.R., Campbell K.P.;	
RT "Sequence similarity of calreticulin with a Ca2(+)-binding protein	
RT that co-purifies with an Ins(1,4,5)P3-sensitive Ca2+ store in HL-60	

RT cella.";  
 RL Biochem. J. 270:545-548(1990).  
 RN [7]  
 RP SEQUENCE OF 18-28.  
 RC TISSUE: Liver;  
 RX MEDLINE-93162045; PubMed 1286669;  
 RA Hochstrasser D.F., Frutiger S., Paquet N., Bairoch A., Ravier F.,  
 Pasquall C., Sanchez J.-C., Tissot J.-D., Bjellqvist B., Vargas R.,  
 Appel R.D., Hughes G.J.;  
 RA Human liver protein map: a reference database established by  
 RT microsequencing and gel comparison.";  
 RL Electrophoresis 13:992-1001(1992).  
 RN [8]  
 RP PARTIAL SEQUENCE OF 25-34; 56-62; 208-221 AND 273-278.  
 RC TISSUE: Keratinocytes;  
 RX MEDLINE-93162043; PubMed 1286667;  
 RA Vandekerckhove J.;  
 RT "Microsequences of 145 proteins recorded in the two-dimensional gel  
 RT protein database of normal human epidermal keratinocytes.";  
 RL Electrophoresis 13:960-969(1992).  
 RN [9]  
 RP SEQUENCE OF 18-26.  
 RC TISSUE: Colon carcinoma;  
 RX MEDLINE-97295306; PubMed 9150948;  
 RA Ji H., Reid G.E., Moritz R.L., Eddes J.S., Burgess A.W., Simpson R.J.;  
 RT "A two-dimensional gel database of human colon carcinoma proteins.";  
 RL Electrophoresis 18:605-613(1997).  
 CC -!- FUNCTION: THIS PROTEIN BINDS CALCIUM. THERE ARE BOTH HIGH AND  
 CC LOW AFFINITY CALCIUM-BINDING SITES.  
 CC -!- SUBUNIT: MONOMER (BY SIMILARITY).  
 CC -!- SUBCELLULAR LOCATION: ENDOPLASMIC RETICULUM LUMEN.  
 CC -!- SIMILARITY: BELONGS TO THE CALRETICULIN FAMILY.  
 CC -!- CAUTION: WAS ORIGINALLY (REF.2) THOUGHT TO BE THE RO AUTOANTIGEN.  
 CC -----  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation  
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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 DR EMBL; M84739; AAA51916.1; -;  
 DR EMBL; M32294; AAA36582.1; -;  
 DR EMBL; AD000092; AAB51176.1; -;  
 DR PIR; A37047; A37047.  
 DR PIR; S11475; S11475.  
 DR PIR; A42330; A42330.  
 DR PIR; A46452; A46452.  
 DR SWISS-2DPAGE; P27797; HUMAN.  
 DR Arthur/Ghent-2DPAGE; 9401; IEF.  
 DR HSC-2DPAGE; P27797; HUMAN.  
 DR MIM; 109091; -;  
 DR InterPro; IPR001580; Calreticulin.  
 DR InterPro; IPR000886; ER target.  
 DR Pfam; PF00262; calreticulin; 1.  
 DR PRINTS; PR00626; CALRETICULIN.  
 DR PRODOM; PD001866; Calreticulin; 1.  
 DR PROSITE; PS00014; ER-TARGET; 1.  
 DR PROSITE; PS00803; CALRETICULIN.1; 1.  
 DR PROSITE; PS00804; CALRETICULIN.2; 1.  
 DR PROSITE; PS00805; CALRETICULIN\_REPEAT; 3.  
 KW Endoplasmic reticulum; Calcium-binding; Repeat; Signal.  
 FT SIGNAL  
 FT CHAIN 1  
 FT 18 417 CALRETICULIN.  
 FT DOMAIN 18 197 N-DOMAIN.  
 FT DOMAIN 198 308 P-DOMAIN.  
 FT DOMAIN 309 417 C-DOMAIN.  
 FT DOMAIN 191 255 4 X APPROXIMATE REPEATS.  
 FT REPEAT 191 202 1-1.  
 FT REPEAT 210 221 1-2.  
 FT REPEAT 227 238 1-3.

FT REPEAT 244 255 1-4.  
 FT DOMAIN 259 297 3 X APPROXIMATE REPEATS.  
 FT REPEAT 259 269 2-1.  
 FT REPEAT 273 283 2-2.  
 FT REPEAT 287 297 2-3.  
 FT DOMAIN 351 408 ASP/GLU/LYS-RICH.  
 FT DISULFID 137 163 BY SIMILARITY.  
 FT SITE 414 417 PREVENT SECRETION FROM ER.  
 FT CONFLICT 35 35 MISSING (IN REF. 3).  
 SQ SEQUENCE 417 AA; 48141 MW; BC37C3C0F1054FB2 CRC64;  
 Query Match 100.0%; Score 971; DB 1; Length 417;  
 Best Local Similarity 100.0%; Pred. No. 4.8e-80;  
 Matches 180; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 EPAVYFKEQFLDGDGWTSRWIESKHKSDFGKFLVSSGKFGYGDDEKDKGLQTSQDARFYAL 60  
 DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 QY 18 EPAVYFKEQFLDGDGWTSRWIESKHKSDFGKFLVSSGKFGYGDDEKDKGLQTSQDARFYAL 77  
 DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 QY 61 SASPEFSSNKGQTLVVQFTVKHEQNIIDCGGYVVKLPNSLDQTDHMDSEYNIMFGPDIC 120  
 DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 QY 78 SASPEFSSNKGQTLVVQFTVKHEQNIIDCGGYVVKLPNSLDQTDHMDSEYNIMFGPDIC 137  
 DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 QY 121 GPCTKKVHVIFNYKGNVNLINKDIRCKDDEFTHLVTLVLRPONTVEYKIDNSQVSGSLE 180  
 DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 QY 138 GPCTKKVHVIFNYKGNVNLINKDIRCKDDEFTHLVTLVLRPONTVEYKIDNSQVSGSLE 197  
 DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 RESULT 2  
 ID CRTX\_RAT STANDARD; PRT; 416 AA.  
 AC P18418; P10452;  
 DT 01-MAR-1989 (Rel. 10, Created)  
 DT 01-NOV-1990 (Rel. 16, Last sequence update)  
 DT 01-NOV-1997 (Rel. 35, Last annotation update)  
 DE CALRETICULIN PRECURSOR (CRP55) (CALREGULIN) (HACBP) (ERP60) (CALBP)  
 DE (CALCIUM-BINDING PROTEIN 3) (CABP3).  
 GN CALR.  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.  
 OX NCBI\_TaxID-10116;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-SPRAGUE-DAWLEY; TISSUE-Brain cortex;  
 RX MEDLINE-90370496; PubMed-2395661;  
 RA Murthy K.K., Banville D., Srikanth C.B., Carrier F., Bell A.,  
 RA Holmes C., Patel Y.C.;  
 RT "Structural homology between the rat calreticulin gene product and  
 RT the Onchocerca volvulus antigen Ral-1.";  
 RL Nucleic Acids Res. 18:4933-4933(1990).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-SPRAGUE-DAWLEY;  
 RX MEDLINE-93202172; PubMed-8453984;  
 RA Nakamura M., Moriya M., Baba T., Michikawa Y., Yamanobe T., Arai K.,  
 RA Okinaga S., Kobayashi T.;  
 RT "An endoplasmic reticulum protein, calreticulin, is transported into  
 RT the acrosome of rat sperm.";  
 RL Exp. Cell Res. 205:101-110(1993).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN SPRAGUE-DAWLEY; TISSUE-Liver;  
 RX MEDLINE-95181573; PubMed-7876339;  
 RA Soennichsen B., Fuehlkrug J., van Nguyen P., Diekmann W.,  
 RA Robinson D.G., Mieskes G.;  
 RT "Retention and retrieval: both mechanisms cooperate to maintain  
 RT calreticulin in the endoplasmic reticulum.";  
 RL J. Cell Sci. 107:2705-2717(1994).  
 RN [4]  
 RP SEQUENCE OF 270-358 FROM N.A.  
 RC STRAIN-SPRAGUE-DAWLEY;

RA Lone Y.C., Bailly A., Latruffe N.;  
 RL Submitted (DEC-1988) to the EMBL/GenBank/DBJ databases.  
 RN (5)  
 RP SEQUENCE OF 18-29.  
 RX MEDLINE=91054414; PubMed=2241926;  
 RA Treves S., de Mattei M., Lanfredi M., Villa A., Green N.M.,  
 RA MacLennan D.H., Meldolesi J., Pozzan T.;  
 RT "Calreticulin is a candidate for a calsequestrin-like function in  
 RT Ca2(+)-storage compartments (calciosomes) of liver and brain.";  
 RL Biochem. J. 271:473-480(1990).  
 RN (6)  
 RP SEQUENCE OF 18-32.  
 RC STRAIN=SPRAGUE-DAWLEY; TISSUE=Testis;  
 RX MEDLINE=92360010; PubMed=1497655;  
 RA Nakamura M., Michikawa Y., Baba T., Okinaga S., Arai K.;  
 RT "Calreticulin is present in the acrosome of spermatids of rat  
 RT testis.";  
 RL Biochem. Biophys. Res. Commun. 186:668-673(1992).  
 RN (7)  
 RP SEQUENCE OF 18-32.  
 RC STRAIN=LEC; TISSUE=Liver;  
 RX MEDLINE=94072621; PubMed=8251535;  
 RA Yokoi T., Nagayama S., Kajiwara R., Kawaguchi Y., Horiuchi R.,  
 RA Kamataki T.;  
 RT "Identification of protein disulfide isomerase and calreticulin as  
 RT autoantigenic antigens in LEC strain of rats.";  
 RL Biochim. Biophys. Acta 1158:339-344(1993).  
 CC -!- FUNCTION: THIS PROTEIN BINDS CALCIUM. THERE ARE BOTH HIGH AND  
 CC LOW AFFINITY CALCIUM-BINDING SITES.  
 CC -!- SUBUNIT: MONOMER (BY SIMILARITY).  
 CC -!- SUBCELLULAR LOCATION: ENDOPLASMIC RETICULUM LUMEN.  
 CC -!- SIMILARITY: BELONGS TO THE CALRETICULIN FAMILY.  
 CC -!- FUNCTION: WAS ORIGINALLY (REF.2) THOUGHT TO BE D-BETA-  
 CC HYDROXYBUTYRATE DEHYDROGENASE.  
 CC -----  
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 CC -----  
 DR EMBL; D78308; BAA1345.1; -;  
 DR EMBL; X53363; CAA37446.1; -;  
 DR EMBL; X13702; CAA31987.1; ALT\_SEQ.  
 DR EMBL; X79327; CAA55890.1; -;  
 DR PIR; S04867; S04867.  
 DR PIR; S11205; S11205.  
 DR PIR; S13045; S13045.  
 DR PIR; A49176; A49176.  
 DR PIR; S45036; S45036.  
 DR PIR; JH0819; JH0819.  
 DR InterPro; IPR001580; Calreticulin.  
 DR InterPro; IPR000886; ER\_target.  
 DR Pfam; PF00262; calreticulin; 1.  
 DR PRINTS; PR00626; CALRETICULIN.  
 DR ProDom; PD001866; Calreticulin; 1.  
 DR PROSITE; PS00014; ER\_TARGET; 1.  
 DR PROSITE; PS00803; CALRETICULIN\_1; 1.  
 DR PROSITE; PS00804; CALRETICULIN\_2; 1.  
 DR PROSITE; PS00805; CALRETICULIN\_REPEAT; 3.  
 DR Endoplasmic reticulum; Calcium-binding; Repeat; Signal.  
 FT SIGNAL 1 17  
 FT CHAIN 18 416 CALRETICULIN.  
 FT DOMAIN 18 197 N-DOMAIN.  
 FT DOMAIN 198 308 P-DOMAIN.  
 FT DOMAIN 309 416 C-DOMAIN.  
 FT DOMAIN 191 255 4 X APPROXIMATE REPEATS.  
 FT REPEAT 191 202 1-1.  
 FT REPEAT 210 221 1-2.  
 FT REPEAT 227 238 1-3.  
 FT REPEAT 244 255 1-4.

FT DOMAIN 259 297 3 X APPROXIMATE REPEATS.  
 FT REPEAT 259 269 2-1.  
 FT REPEAT 273 283 2-2.  
 FT REPEAT 287 297 2-3.  
 FT DOMAIN 351 407 ASP/GLU/LYS-RICH.  
 FT DISULFID 137 163 BY SIMILARITY.  
 FT SITE 413 416 PREVENT SECRETION FROM ER.  
 SQ SEQUENCE 416 AA; 47995 MW; 256713CED31A2970 CRC64;  
 Query Match 96.1%; Score 933; DB 1; Length 416;  
 Best Local Similarity 94.4%; Pred. No. 1.2e-76;  
 Matches 170; Conservative 5; Mismatches 5; Indels 0; Gaps 0;  
 Qy 1 EPAYVFEQFLDGDGWTSRWIESKHKSDFGKFLVSSGKFYGDDEKDKGLQTSQDARFYAL 60  
 :||:||||||| ||:||||||| ||:||||||| ||:||||||| ||:||||||| ||:|||||||  
 Db 18 DPAYVFEQFLDGDGDAWTRWVESKHKSDFGKFLVSSGKFYGDQEKDKGLQTSQDARFYAL 77  
 Qy 61 SASPEPFSNKGQTLVVQFTVKHEQNIIDCGGGYVKLFPPNSLDQTMHGDSSEYNIMFGPDIC 120  
 || ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 Db 78 SARPEPFSNKGQTLVVQFTVKHEQNIIDCGGGYVKLFPPGGLDQKDMHGDSEYNIMFGPDIC 137  
 Qy 121 GPGTKKVVHVIENYKGNVLIINKDIRCKDDETHLYTLVLRPNTVEVKIDNSQVSSGLE 180  
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 Db 138 GPGTKKVVHVIENYKGNVLIINKDIRCKDDETHLYTLVLRPNTVEVKIDNSQVSSGLE 197  
 RESULT 3  
 ID CRTG\_RABIT STANDARD; PRT; 418 AA.  
 AC P15253;  
 DT 01-APR-1990 (Rel. 14, Created)  
 DT 01-APR-1990 (Rel. 14, Last sequence update)  
 DT 01-OCT-1996 (Rel. 34, Last annotation update)  
 DE CALRETICULIN PRECURSOR (CRP55) (CALREGULIN) (HACBP) (ERP60).  
 GN CALR.  
 OS Oryctolagus cuniculus (Rabbit).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.  
 OX NCBI\_TaxID=9986;  
 RN [1]  
 RC SEQUENCE FROM N.A.  
 RP TISSUE=Slow-twitch skeletal muscle;  
 RX MEDLINE=90094320; PubMed=2600080;  
 RA Fliegel L., Burns K., MacLennan D.H., Reithmeier R.A.F., Michalak M.;  
 RT "Molecular cloning of the high affinity calcium-binding protein  
 RT (calreticulin) of skeletal muscle sarcoplasmic reticulum.";  
 RL J. Biol. Chem. 264:21522-21528(1989).  
 RN [2]  
 RC SEQUENCE FROM N.A.  
 RP TISSUE=Fast-twitch skeletal muscle;  
 RX MEDLINE=91282795; PubMed=2059224;  
 RA Fliegel L., Michalak M.;  
 RT "Fast-twitch and slow-twitch skeletal muscles express the same  
 RT isoform of calreticulin.";  
 RL Biochem. Biophys. Res. Commun. 177:979-984(1991).  
 RN [3]  
 RC SEQUENCE OF 18-36.  
 RX MEDLINE=91054414; PubMed=2241926;  
 RA Treves S., de Mattei M., Lanfredi M., Villa A., Green N.M.,  
 RA MacLennan D.H., Meldolesi J., Pozzan T.;  
 RT "Calreticulin is a candidate for a calsequestrin-like function in  
 RT Ca2(+)-storage compartments (calciosomes) of liver and brain.";  
 RL Biochem. J. 271:473-480(1990).  
 RN [4]  
 RP SEQUENCE OF 18-46.  
 RX MEDLINE=91201375; PubMed=2016321;  
 RA Milner R.E., Baksh S., Shemanko C., Carpenter M.R., Smillie L.,  
 RA Vance J.E., Opas M., Michalak M.;  
 RT "Calreticulin, and not calsequestrin, is the major calcium binding  
 RT protein of smooth muscle sarcoplasmic reticulum and liver endoplasmic  
 RT reticulum.";  
 RL J. Biol. Chem. 266:7155-7165(1991).

RR PARTIAL SEQUENCE.  
RC TISSUE: Lung;  
RX MEDLINE-94002038; PubMed 1911780;  
RT Guan S., Fallick A.M., Williams D.E., Cashman J.R.;  
RT "Evidence for complex formation between rabbit lung flavin-containing  
RL monooxygenase and calreticulin."  
RL Biochemistry 30:9892-9900(1991).  
CC -|- FUNCTION: THIS PROTEIN BINDS CALCIUM. THERE ARE BOTH HIGH AND  
CC LOW AFFINITY CALCIUM-BINDING SITES.  
CC -|- SUBUNIT: MONOMER (BY SIMILARITY).  
CC -|- SUBCELLULAR LOCATION: ENDOPLASMIC RETICULUM LUMEN.  
CC -|- SIMILARITY: BELONGS TO THE CALRETICULIN FAMILY.  
CC -----  
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CC -----  
DR EMBL; J05138; AAA31188.1; -;  
DR PIR; A34154; A34154.  
DR PIR; C33208; C33208.  
DR PIR; D33208; D33208.  
DR PIR; E33208; E33208.  
DR PIR; F33208; F33208.  
DR PIR; S13046; S13046.  
DR PIR; S13047; S13047.  
DR InterPro; IPR001580; Calreticulin.  
DR InterPro; IPR000886; ER-target.  
DR Pfam; PF00262; calreticulin; 1.  
DR PRINTS; PR00626; CALRETICULIN.  
DR PRODOM; PD001866; Calreticulin; 1.  
DR PROSITE; PS00014; ER-TARGET; 1.  
DR PROSITE; PS00803; CALRETICULIN\_1; 1.  
DR PROSITE; PS00804; CALRETICULIN\_2; 1.  
DR PROSITE; PS00805; CALRETICULIN\_REPEAT; 3.  
KW Endoplasmic reticulum; Calcium-binding; Repeat; Signal.  
FT SIGNAL 1 17  
FT CHAIN 18 418 CALRETICULIN.  
FT DOMAIN 18 197 N-DOMAIN.  
FT DOMAIN 198 308 P-DOMAIN.  
FT DOMAIN 309 418 C-DOMAIN.  
FT DOMAIN 191 255 4 X APPROXIMATE REPEATS.  
FT REPEAT 191 202 1-1.  
FT REPEAT 210 221 1-2.  
FT REPEAT 227 238 1-3.  
FT REPEAT 244 255 1-4.  
FT DOMAIN 259 297 3 X APPROXIMATE REPEATS.  
FT REPEAT 259 269 2-1.  
FT REPEAT 273 283 2-2.  
FT REPEAT 287 297 2-3.  
FT DOMAIN 351 408 ASP/GLU/LYS-RICH.  
FT DISULFID 137 163 BY SIMILARITY.  
FT SITE 415 418 PREVENT SECRETION FROM ER.  
FT VARIANT 35 35 E -> D. (IN REF. 5).  
FT CONFLICT 90 90 P -> T. (IN REF. 5).  
SQ SEQUENCE 418 AA; 48275 MW; B6082B689DC763A6 CRC64;

Query Match 95.9%; Score 931; DB 1; Length 418;  
Best Local Similarity 95.6%; Pred. No. 1.9e-76;  
Matches 172; Conservative 1; Mismatches 7; Indels 0; Gaps 0;  
QY 1 EPVAVYFKQFLDGDGWTGRWIESKHKSDFGKFLVSSGKFGYGDDEKDKGLQTSQDARFYAL 60  
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DB 18 EPVVYFKQFLDGDGWTGRWIESKHKSDFGKFLVSSGKFGYGDDEKDKGLQTSQDARFYAL 77  
QY 61 SASFPFPNKGQTLVQFTVKHEQNDICGGGYVKFLFPNSLDQTDHMGSEYNIMFGPDIC 120  
|||  
DB 78 SARFPFPNKGQTLVQFTVKHEQNDICGGGYVKFLFPNSLDQTDHMGSEYNIMFGPDIC 137

QY 121 GPGTKKVVHFIENYKGNVLINKDIRKDDFTHLYTLIVRPDNTYEVKIDNSQVSGSLE 180  
DB 138 GPGTKKVVHFIENYKGNVLINKDIRKDDFTHLYTLIVRPDNTYEVKIDNSQVSGSLE 197  
RESULT 4  
CRT1\_BOVIN  
ID CRT1\_BOVIN STANDARD; PRT; 400 AA.  
AC P52193;  
DT 01-OCT-1996 (Rel. 34, Created)  
DT 01-OCT-1996 (Rel. 34, Last sequence update)  
DT 01-OCT-1996 (Rel. 34, Last annotation update)  
DE CALRETICULIN, BRAIN ISOFORM 1 (CRP55) (CALREGULIN) (HACBP).  
OS Bos taurus (Bovine).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
OC Bovidae; Bovinae; Bos.  
OX NCBI\_TaxID:9913;  
RN [1]  
RP SEQUENCE.  
RC TISSUE: Brain;  
RX MEDLINE-94183174; PubMed 8135753;  
RA Matsuo K., Seta K., Yamakawa Y., Okuyama T., Shinoda T.;  
RT "Covalent structure of bovine brain calreticulin."  
RL Biochem. J. 298:435-442(1994).  
CC -|- FUNCTION: THIS PROTEIN BINDS CALCIUM. THERE ARE BOTH HIGH AND  
CC LOW AFFINITY CALCIUM-BINDING SITES.  
CC -|- SUBUNIT: MONOMER.  
CC -|- SUBCELLULAR LOCATION: ENDOPLASMIC RETICULUM LUMEN.  
CC -|- SIMILARITY: BELONGS TO THE CALRETICULIN FAMILY.  
DR InterPro; IPR001580; Calreticulin.  
DR Pfam; PF00262; calreticulin; 1.  
DR PRINTS; PR00626; CALRETICULIN.  
DR PRODOM; PD001866; Calreticulin; 1.  
DR PROSITE; PS00014; ER-TARGET; 1.  
DR PROSITE; PS00803; CALRETICULIN\_1; 1.  
DR PROSITE; PS00804; CALRETICULIN\_2; 1.  
DR PROSITE; PS00805; CALRETICULIN\_REPEAT; 3.  
KW Endoplasmic reticulum; Calcium-binding; Repeat; Glycoprotein.  
FT DOMAIN 1 180 N-DOMAIN.  
FT DOMAIN 181 291 P-DOMAIN.  
FT DOMAIN 292 400 C-DOMAIN.  
FT DOMAIN 174 238 4 X APPROXIMATE REPEATS.  
FT REPEAT 174 185 1-1.  
FT REPEAT 193 204 1-2.  
FT REPEAT 210 221 1-3.  
FT REPEAT 227 238 1-4.  
FT DOMAIN 242 280 3 X APPROXIMATE REPEATS.  
FT REPEAT 242 252 2-1.  
FT REPEAT 256 266 2-2.  
FT REPEAT 270 280 2-3.  
FT DOMAIN 334 390 ASP/GLU/LYS-RICH.  
FT DISULFID 120 146 N-LINKED (GLCNAC...).  
FT CARBOHYD 162 162 PREVENT SECRETION FROM ER (POTENTIAL).  
FT SITE 397 400  
SQ SEQUENCE 400 AA; 46381 MW; 7D4B68DFC689EEF1 CRC64;

Query Match 95.8%; Score 930; DB 1; Length 400;  
Best Local Similarity 95.0%; Pred. No. 2.2e-76;  
Matches 171; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY 1 EPVAVYFKQFLDGDGWTGRWIESKHKSDFGKFLVSSGKFGYGDDEKDKGLQTSQDARFYAL 60  
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DB 1 DPTVYFKQFLDGDGWTGRWIESKHKSDFGKFLVSSGKFGYGDDEKDKGLQTSQDARFYAL 60  
QY 61 SASFPFPNKGQTLVQFTVKHEQNDICGGGYVKFLFPNSLDQTDHMGSEYNIMFGPDIC 120  
|||  
DB 61 SARFPFPNKGQTLVQFTVKHEQNDICGGGYVKFLFPNSLDQTDHMGSEYNIMFGPDIC 120  
QY 121 GPGTKKVVHFIENYKGNVLINKDIRKDDFTHLYTLIVRPDNTYEVKIDNSQVSGSLE 180



FT	DOMAIN	198	308	P-DOMAIN.
FT	DOMAIN	309	416	C-DOMAIN.
FT	DOMAIN	391	255	4 X APPROXIMATE REPEATS.
FT	REPEAT	191	202	1-1.
FT	REPEAT	210	221	1-2.
FT	REPEAT	227	238	1-3.
FT	REPEAT	227	238	1-3.
FT	REPEAT	244	255	1-4.
FT	DOMAIN	259	297	3 X APPROXIMATE REPEATS.
FT	REPEAT	259	269	2-1.
FT	REPEAT	273	283	2-2.
FT	REPEAT	287	297	2-3.
FT	DOMAIN	351	407	ASP/GLU/LYS-RICH.
FT	DISULFID	137	163	BY SIMILARITY.
FT	SITE	413	416	PREVENT SECRETION FROM ER.
SQL	SEQUENCE	416 AA;	47994 MW;	24C03B00913408D8 CRC64;

  

Query Match	95.8%;	Score 930;	DB 1;	Length 416;
Best Local Similarity	94.4%;	Pred. No. 2.3e-76;		
Matches 170;	Conservative	5;	Mismatches	5; Indels 0; Gaps 0;

  

QY	1	EPAVFYKEQFLDGGWTSRWIESKHKSDFGKFVLSSSGKFYGDSEKDKGLQTSQDARFYAL	60
DB	18	DPAIYFKEQFLDGGWTSRWIESKHKSDFGKFVLSSSGKFYGDSEKDKGLQTSQDAREYAL	77
QY	61	SASFEPFSNKGQTLVQFTVKYHEONIDCGGYYVKLFPSNLSLQDTDMHGDSSEYNINFGPDIC	120
DB	78	SAKFEPSNKGQTLVQFTVKYHEONIDCGGYYVKLFPSNLSLQDTDMHGDSSEYNINFGPDIC	137
QY	121	PGGTGKVVHVFNYKGVKNVLINKDRCKDDETHLYTLTVRPDNTYEVKIDNSQVESGSL	180
DB	138	PGGTGKVVHVFNYKGVKNVLINKDRCKDDETHLYTLTVRPDNTYEVKIDNSQVESGSL	197

  

RESULT	6
CRIC_DROME	
ID	CRIC_DROME
STANDARD;	PRT;
406 AA.	
AC	P29413; Q9VHA3;
DT	01-APR-1993 (Rel. 25, Created)
DT	01-OCT-1993 (Rel. 27, Last sequence update)
DT	20-AUG-2001 (Rel. 40, Last annotation update)
DE	CALRETICULIN PRECURSOR (CRP55) (CALREGULIN) (HACBP).
GN	CRIC OR CG9429.
OS	Drosophila melanogaster (Fruit fly).
OC	Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC	Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC	Ephyaridea; Drosophilidae; Drosophila.
OX	NCBI_TaxID=7227;
RN	[1]
RP	SEQUENCE FROM N.A.
RX	MEDLINE=93208374; PubMed=1296819;
SM	Smith M.J.;
RT	"Nucleotide sequence of a Drosophila melanogaster gene encoding a
RT	calreticulin homologue."
RL	DNA Seq. 3:247-250(1992).
RL	[2]
RC	SEQUENCE FROM N.A.
RC	STRAIN=BERKELEY.
RX	MEDLINE=20196006; PubMed=10731132;
RA	Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA	Ananides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA	George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA	Sutton G.G., Wortman J.R., Vandell M.D., Zhang Q., Chen L.X.,
RA	Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA	Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA	Abriel J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA	Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA	Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA	Borkova D., Botchan M.R., Bouck J., Brockstein P., Brotter P.,
RA	Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA	Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA	de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA	Dodson K., Dou L.E., Downes M., Duquenois R., Dunkov B.C., Dunn P.,





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FT REPEAT 211 222 1-2.
FT REPEAT 227 238 1-3.
FT REPEAT 246 257 1-4.
FT DOMAIN 260 298 3 X 11 AA APPROXIMATE REPEATS.
FT REPEAT 260 270 2-1.
FT REPEAT 274 284 2-2.
FT REPEAT 288 298 2-3.
FT DISULFID 105 137 BY SIMILARITY.
FT SITE 421 424 PREVENT SECRETION FROM ER (POTENTIAL).
SQ SEQUENCE 424 AA: 48350 MW: BAP273694FB6FC37 CRC64;

Query Match 55.3%; Score 537; DB 1; Length 424;
Best Local Similarity 57.2%; Pred. No. 4.7e-41;
Matches 103; Conservative 36; Mismatches 33; Indels 8; Gaps 7;

QY 4 VYKPEFLDGDGWTWSWIESK-HKSD--FGKFLSSGKFGDEKDKGLQTSODARFYAL 60
DB 21 VHPKDTF-DND-WESRWVSDMHKEDGSKGLVHTAGKWFGENQ-KGIQTSedarFYAV 77
QY 61 SASPEFSNKGOTLVQFTVKHEQNDGCGYVVKLFPSNLDQTDHMGDSEYNIMFGPDIC 120
DB 78 SARFSPSNKGDLVQYTVKNEQKVDGCGSYIKLLPSKLDQSAFDGSESEYSIMFGPDVC 137
QY 121 GPCTKKVHVIFNYKGNVLINKDI-RCKDDEFTHLTVLRPDPNTYEVKIDNSQVESGSL 179
DB 138 G-ASKRVHVLNKGKHLIKKEINKVETDQLTHQYTLVISPDPNTYVNLVDNKEIQAGNL 196

RESULT 10
CRTC_EUGGR
ID CRTC_EUGGR STANDARD; PRT; 401 AA.
AC Q92NY3;
DT 20-AUG-2001 (Rel. 40, Created)
DT 20-AUG-2001 (Rel. 40, Last sequence update)
DE CALRETICULIN PRECURSOR.
OS Euglena gracilis.
OC Eukaryota; Euglenozoa; Euglenida; Euglenales; Euglena.
OX NCBI_TaxID 3039;
RN [1]
SEQUENCE FROM N.A.
RA Navaziz L., Balidan B., Martin W., Mariani P.;
RT "Evidence for conservation of a calcium homeostat component: purification characterization and cloning of calreticulin from Euglena gracilis."
KT Submitted (DEC-1996) to the EMBL/GenBank/DBJ databases.
RT Submitted (DEC-1996) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: THIS PROTEIN BINDS CALCIUM. THERE ARE BOTH HIGH AND LOW AFFINITY CALCIUM-BINDING SITES (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: ENDOPLASMIC RETICULUM LUMEN (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE CALRETICULIN FAMILY.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).
CC EMBL; Y09816; CAA70945.1;
CC InterPro; IPR001580; Calreticulin.
CC InterPro; IPR000886; ER-target.
CC Pfam; PF00262; Calreticulin; 1.
CC PRINTS; P000626; CALRETICULIN.
CC PROSITE; PS00014; ER-TARGET; 1.
CC PROSITE; PS00803; CALRETICULIN_1; 1.
CC PROSITE; PS00804; CALRETICULIN_2; 1.
CC PROSITE; PS00805; CALRETICULIN_REPEAT; 1.
CC Endoplasmic reticulum; Calcium-binding; Repeat; Signal.
CC SIGNAL 1 18 POTENTIAL.
CC CHAIN 19 401 CALRETICULIN.
FT CARBOHYD 57 57
FT CARBOHYD 157 157
FT SITE 413 416
SQ SEQUENCE 416 AA: 48136 MW: 565FEC3489F77CA7 CRC64;
```

```
FT SITE 398 401 PREVENT SECRETION FROM ER (POTENTIAL).
SQ SEQUENCE 401 AA: 45910 MW: 056B074C16292674 CRC64;

Query Match 55.1%; Score 535.5; DB 1; Length 401;
Best Local Similarity 56.7%; Pred. No. 6e-41;
Matches 101; Conservative 30; Mismatches 42; Indels 5; Gaps 4;

QY 4 VYKPEFLDGDGWTWSWIESKHSKDFGKFLSSGKFGDEKDKGLQTSODARFYALSAS 63
DB 20 IYKETF--EPDWETRWTHSTAKSDYKFKLTSGKFGYDKAKDAGIQTSDAKFYAISP 77
QY 64 F-EPPFNKGOTLVQFTVKHEQNDGCGYVVKLFPSNLDQTDHMGDSEYNIMFGPDICGP 122
DB 78 IASSFSEKEDLVQFSVKEHQDIDCGGYLKLLP-SVDAAKFTGDTPHIIFGPDICG- 135
QY 123 GTRKKVHVIFNYKGNVLINKDI-RCKDDEFTHLTVLRPDPNTYEVKIDNSQVESGSL 180
DB 136 ATKKIHFILTYKGNLLKKKEPCRTDTLSHTVTAVIKADRTVEVLVDQVKKESGTL 193

RESULT 11
CRTC_BETVU
ID CRTC_BETVU STANDARD; PRT; 416 AA.
AC O81919;
DT 20-AUG-2001 (Rel. 40, Created)
DT 20-AUG-2001 (Rel. 40, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE CALRETICULIN PRECURSOR.
OS Beta vulgaris (Sugar beet).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Caryophyllidae; Caryophyllales; Chenopodiaceae; Beta.
OX NCBI_TaxID 3555;
RN [1]
SEQUENCE FROM N.A.
RC STRAIN-VV-D/2R5; TISSUE=Leaf;
RA Viereck R.;
RT "Nucleotide sequence from sugar beet calreticulin."
RL Submitted (OCT-1997) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: THIS PROTEIN BINDS CALCIUM. THERE ARE BOTH HIGH AND LOW AFFINITY CALCIUM-BINDING SITES (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: ENDOPLASMIC RETICULUM LUMEN (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE CALRETICULIN FAMILY.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).
CC EMBL; AJ002057; CAA05161.1;
CC Mendel; 32549; Betvu.1166;32549
CC InterPro; IPR001580; Calreticulin.
CC InterPro; IPR000886; ER-target.
CC Pfam; PF00262; calreticulin; 1.
CC PRINTS; P000626; CALRETICULIN.
CC PRODOM; PD001866; Calreticulin; 1.
CC PROSITE; PS00014; ER-TARGET; 1.
CC PROSITE; PS00803; CALRETICULIN_1; 1.
CC PROSITE; PS00804; CALRETICULIN_2; 1.
CC PROSITE; PS00805; CALRETICULIN_REPEAT; 2.
CC Endoplasmic reticulum; Calcium-binding; Repeat; Signal; Glycoprotein.
CC SIGNAL 1 25 POTENTIAL.
CC CHAIN 26 416 CALRETICULIN.
CC CARBOHYD 57 57
CC CARBOHYD 157 157
CC SITE 413 416
SQ SEQUENCE 416 AA: 48136 MW: 565FEC3489F77CA7 CRC64;
```

[illegible]

Query Match 53.8%; Score 522.5; DB 1; Length 421;

Best Local Similarity 55.6%; Pred. NO. 9.4e-40;  
Matches 109; Conservative 12; Mismatches 30; Indels 45; Gaps 4;

QY	1	EPAVYFKEQFLDGDGWTSRWIESKHKSD-----FGKFVLSSGKFGYDDEE	44
Db	35	EETVFSEQFLT-----LDLKYRASKLSSIREALSMKVGIIENFCFSEISLQESI	86
QY	45	KDKGLQTSODARFYALSASFEPFSNKGQTLVVQFTVKHEQNIDCGGGYVKLFPNSLDQTD	104
Db	87	KSHGRRT-----LVGCCSPWGHE-----EQNIDCGGGYVNVFPAGLDQTD	125
QY	105	MHGDSEYNIMFGPDICGPGTKKVHVIFNYKGNVLINKDIRCKDDETHLYTLIVRPDNT	164
Db	126	MHGDSEYNIMFGPDICGPGTKKVHVIFNYKGNVLINKDIRCKDDETHLYTLIVRPNT	185
QY	165	YEVKIDNSOVESGSLE	180
Db	186	YEVKIDNSOVESGSLE	201

Search completed: January 9, 2002, 15:12:14  
Job time: 656 sec





GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: January 14, 2002, 08:48:49 ; Search time 23.38 Seconds  
(without alignments)  
570.282 Million cell updates/sec

Title: US-09-828-000-3  
Perfect score: 180  
Sequence: 1 EPAYVKEQFLDGGWTSRW.....PDNTYEVKIDNSQVESGSL 180

Scoring table:  
OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 522463 seqs, 74073290 residues

Word size : 18  
Total number of hits satisfying chosen parameters: 14

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database : A\_Geneseq\_1101.\*  
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2: /SID88/gcgdata/geneseq/geneseqp/AA1981.DAT.\*  
3: /SID88/gcgdata/geneseq/geneseqp/AA1982.DAT.\*  
4: /SID88/gcgdata/geneseq/geneseqp/AA1983.DAT.\*  
5: /SID88/gcgdata/geneseq/geneseqp/AA1984.DAT.\*  
6: /SID88/gcgdata/geneseq/geneseqp/AA1985.DAT.\*  
7: /SID88/gcgdata/geneseq/geneseqp/AA1986.DAT.\*  
8: /SID88/gcgdata/geneseq/geneseqp/AA1987.DAT.\*  
9: /SID88/gcgdata/geneseq/geneseqp/AA1988.DAT.\*  
10: /SID88/gcgdata/geneseq/geneseqp/AA1989.DAT.\*  
11: /SID88/gcgdata/geneseq/geneseqp/AA1990.DAT.\*  
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14: /SID88/gcgdata/geneseq/geneseqp/AA1993.DAT.\*  
15: /SID88/gcgdata/geneseq/geneseqp/AA1994.DAT.\*  
16: /SID88/gcgdata/geneseq/geneseqp/AA1995.DAT.\*  
17: /SID88/gcgdata/geneseq/geneseqp/AA1996.DAT.\*  
18: /SID88/gcgdata/geneseq/geneseqp/AA1997.DAT.\*  
19: /SID88/gcgdata/geneseq/geneseqp/AA1998.DAT.\*  
20: /SID88/gcgdata/geneseq/geneseqp/AA1999.DAT.\*  
21: /SID88/gcgdata/geneseq/geneseqp/AA2000.DAT.\*  
22: /SID88/gcgdata/geneseq/geneseqp/AA2001.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	180	100.0	180	21	Human vasostatin (
2	180	100.0	400	21	Recombinant human
3	180	100.0	417	10	60 kD Ro (Ro/SSA)
4	180	100.0	417	21	Human MBP-calretic
5	162	90.0	417	20	Calreticulin. Hom
6	77	42.8	401	18	Calreticulin. Hom
7	61	33.9	61	21	Recombinant human
8	60	33.3	60	21	Recombinant human
9	60	33.3	280	21	Recombinant delc-
10	49	27.2	49	21	Recombinant human
11	36	20.0	122	20	Human cC1qR bindin

12 36 20.0 122 20 AAY00926 Rat cC1qR binding  
13 19 10.6 122 20 AAY00925 Mouse cC1qR bindin  
14 19 10.6 336 12 AAR12312 Partial sequence o

ALIGNMENTS

RESULT 1  
AAY92351  
ID AAY92351 standard; Protein; 180 AA.

XX AAY92351;

DT 10-AUG-2000 (first entry)

DE Human vasostatin (calreticulin N-terminal 180 amino acids).

XX MBP-calreticulin; maltose binding protein; vasostatin; N-terminal;  
KW angio genesis; inhibition; endothelial cell; anti-angiogenic;  
KW neuroprotective; anti-diabetic; cytostatic; dermatological; hepatic;  
KW immunosuppressive; anti-inflammatory; anti-atherosclerotic;  
KW gastrointestinal; anti-arthritis; ophthalmic.

OS Homo sapiens.

OS Synthetic.

PN WO200020577-A1.

PD 13-APR-2000.

PF 05-OCT-1999; 99WO-US23240.

PR 06-OCT-1998; 98US-0103438.

PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.

XX Tosato G, Pike SE, Yao L;

PI WPI; 2000-303767/26.

PT Inhibiting endothelial cell growth and angiogenesis using calreticulin,  
useful for suppressing tumor growth

PS Claim 4; Page 82; 99pp; English.

CC A novel method of inhibiting endothelial cell growth comprises  
contacting the cells with calreticulin (or its fragments/variants).  
CC Fragments of calreticulin causes at least 40% inhibition of angiogenesis,  
CC tumor growth and/or endothelial cell growth (claimed). The method may be  
CC used for inhibiting angiogenesis in a patient. The angiogenesis is  
CC associated with a disease other than a tumor that is associated with  
CC neovascularization (e.g. diabetic neuropathy, retrolental fibroplasia,  
CC trachoma, neovascular glaucoma, psoriasis, angiofibromas, immune  
CC inflammation, atherosclerosis, excessive wound repair, retinal  
CC neovascularization, macular degeneration, corneal graft rejection,  
CC contact lens overwear, Crohn's disease, non-immune inflammation,  
CC rheumatoid arthritis, systemic lupus erythematosus, thyroiditis,  
CC Goodpasture's syndrome, systemic vasculitis, scleroderma, Sjorgen's  
CC syndrome, sarcoidosis and primary biliary cirrhosis). The method may  
CC also be used for treating/inhibiting tumor growth especially  
CC Kaposi's sarcoma (claimed).

XX Sequence 180 AA;

Query Match 100.0%; Score 180; DB 21; Length 180;  
Best Local Similarity 100.0%; Pred. No. 2e-187;  
Matches 180; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EPAYVKEQFLDGGWTSRWIESKHKSDFKFLVSSGKFGYDEKDKGLQTSQDARYAL 60

DB 1 epayvkeqfldgdtwtsrwieskhksdfgflvlsagkfygdeekdkgltsqdarfyal 60

```
QY 61 SASFPFNSKGGTLVQFTVKHEQNIIDCGGYYKLFPSNSLQDTMHGSEYNIMFGPDIC 120
|||||
Db 61 sasfepfnskggtlvvqftvkheqnidcggyvklfpnsldqtdmhgdsenimfgpdic 120
|||||
QY 121 GPGTKKVHVIFNYKGNVLINKDKDEFFHLTYLTVRPDNTYEVKIDNSQVSGSLE 180
|||||
Db 121 gpgtkkvhvifnykgknvlinkdirckddefchlyllvvpdntyevkidnsqvesgsl 180
|||||

RESULT 2
AA923350
ID AAY923350 standard; Protein: 400 AA.
XX
AC AAY923350;
XX
DT 10-AUG-2000 (first entry)
XX
DE Recombinant human MBP-Calreticulin.
XX
KW MBP-calreticulin; maltose binding protein; angiogenesis; inhibition;
KW endothelial cell; anti-angiogenic; neuroprotective; antidiabetic;
KW cytostatic; dermatological; immunosuppressive; antiinflammatory; hepatic;
KW anti-atherosclerotic; gastrointestinal; anti-arthritis; ophthalmic.
XX
OS Homo sapiens.
XX
PN WO200020577-A1.
XX
PD 13-APR-2000.
XX
PF 05-OCT-1999; 99WO-US23240.
XX
PR 06-OCT-1998; 98US-0103438.
XX
PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX
PI Tosato G, Pike SE, Yao L;
XX
DR WPI; 2000-303767/26.
DR N-PSDB; AAA09346, AAA09347.
XX
PT Inhibiting endothelial cell growth and angiogenesis using calreticulin,
XX useful for suppressing tumor growth
XX
PS Claim 4; Page 80-81; 99pp; English.
XX
CC Recombinant human MBP-calreticulin comprises the sequence of human
CC calreticulin (see AAY92349) without the 17 N-terminal amino acids.
CC A novel method of inhibiting endothelial cell growth comprises
CC contacting the cells with calreticulin (or its fragments/variants).
CC Fragments of calreticulin causes at least 40% inhibition of
CC angiogenesis, tumor growth and/or endothelial cell growth (claimed). The
CC method may be used for inhibiting angiogenesis in a patient. The
CC angiogenesis is associated with a disease other than a tumor that is
CC associated with neovascularization (e.g. diabetic neuropathy, retrolental
CC fibroplasia, trachoma, neovascular glaucoma, psoriasis, angiofibromas,
CC immune inflammation, atherosclerosis, excessive wound repair, retinal
CC neovascularization, macular degeneration, corneal graft rejection,
CC contact lens overwear, Crohn's disease, non-immune inflammation,
CC rheumatoid arthritis, systemic lupus erythematosus, thyroiditis,
CC Goodpasture's syndrome, systemic vasculitis, scleroderma, Sjorgen's
CC syndrome, sarcoidosis and primary biliary cirrhosis). The method may
CC also be used for treating/inhibiting tumor growth especially
CC Kaposi's sarcoma (claimed).
XX
SQ Sequence 400 AA;
```

```
Query Match 100.0%; Score 180; DB 21; Length 400;
Best Local Similarity 100.0%; Pred. No. 4.1e-187;
Matches 180; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
QY 1 EPAYVFKQFLDGDGWTGRWIESKHKSDFKFLVSSGKFYGDDEKDKGLQTSQDARFYAL 60
|||||
Db 1 epavyfkeqfldgdgwtarwieskhksdfgkfvlssgkfygdeekdkgltsqdarfyal 60
|||||
QY 61 SASFPFNSKGGTLVQFTVKHEQNIIDCGGYYKLFPSNSLQDTMHGSEYNIMFGPDIC 120
|||||
Db 61 sasfepfnskggtlvvqftvkheqnidcggyvklfpnsldqtdmhgdsenimfgpdic 120
|||||
QY 121 GPGTKKVHVIFNYKGNVLINKDKDEFFHLTYLTVRPDNTYEVKIDNSQVSGSLE 180
|||||
Db 121 gpgtkkvhvifnykgknvlinkdirckddefchlyllvvpdntyevkidnsqvesgsl 180
|||||

RESULT 3
AAP92276
ID AAP92276 standard; protein: 417 AA.
XX
AC AAP92276;
XX
DT 23-FEB-1990 (first entry)
XX
DE 60 kD Ro (Ro/SSA) antigen.
XX
KW Sjorens syndrome; systemic lupus erythematosus.
XX
OS Synthetic.
XX
PN WO8909273-A.
XX
PD 05-OCT-1989.
XX
PF 22-MAR-1989; 89WO-US01213.
XX
PR 22-MAR-1988; 88US-0171634.
XX
PA (TEXA ) UNIV OF TEXAS SYST.
XX
PI Sontheimer RD, Capra JD, McCauliffe DP;
XX
DR WPI; 1989-309537/42.
DR N-PSDB; AAP92276.
XX
PT DNA sequences encoding antigenic epitope(s) of Ro 60 kD autoantigen
XX - used in immunoassays to detect rheumatic disease
XX
PS Disclosure; Fig 2; 88pp; English.
XX
CC Synthetic peptides corresp. to an epitopic core of Ro antigen are
CC expressed recombinantly to detect autoantibodies, for identification
CC of autoimmune diseases. These epitopes are AAs 24-36, 23-36, 188-209,
CC or 241-255. The peptides may be substd. for ribonucleoprotein particle
CC antigens.
XX
SQ Sequence 417 AA;
```

```
Query Match 100.0%; Score 180; DB 10; Length 417;
Best Local Similarity 100.0%; Pred. No. 4.2e-187;
Matches 180; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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|||||
Db 18 epavyfkeqfldgdgwtarwieskhksdfgkfvlssgkfygdeekdkgltsqdarfyal 77
|||||
QY 61 SASFPFNSKGGTLVQFTVKHEQNIIDCGGYYKLFPSNSLQDTMHGSEYNIMFGPDIC 120
|||||
Db 78 sasfepfnskggtlvvqftvkheqnidcggyvklfpnsldqtdmhgdsenimfgpdic 137
|||||
QY 121 GPGTKKVHVIFNYKGNVLINKDKDEFFHLTYLTVRPDNTYEVKIDNSQVSGSLE 180
|||||
Db 138 gpgtkkvhvifnykgknvlinkdirckddefchlyllvvpdntyevkidnsqvesgsl 197
|||||
```

```
RESULT 4.
AA92349
ID AAY92349 standard; Protein; 417 AA.
XX
AC AAY92349;
XX
DT 10-AUG-2000 (first entry)
XX
DE Human MBP-calreticulin.
XX
KW MBP-calreticulin; maltose binding protein; angiogenesis; inhibition;
KW endothelial cell; anti-angiogenic; neuroprotective; antidiabetic;
KW cytotatic; dermatological; immunosuppressive; antiinflammatory; hepatic;
KW anti-atherosclerotic; gastrointestinal; anti-arthritis; ophthalmic.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Peptide 1..17
FT /label= signal_peptide
FT Protein 18
FT /label= mature_protein
XX
PN WO200020577-A1.
XX
PD 13-APR-2000.
XX
PF 05-OCT-1999; 99WO-US23240.
XX
PR 06-OCT-1998; 98US-0103438.
XX
PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX
PI Tosato G, Pike SE, Yao L;
XX
DR WPI; 2000-303767/26.
XX
DR N-PSDB; AAA09346, AAA09347.
XX
PT Inhibiting endothelial cell growth and angiogenesis using calreticulin,
PT useful for suppressing tumor growth
XX
PS Disclosure; Page 79-80; 99pp; English.
XX
CC A novel method of inhibiting endothelial cell growth comprises
CC contacting the cells with calreticulin (or its fragments/variants).
CC Fragments of calreticulin causes at least 40% inhibition of angiogenesis,
CC tumor growth and/or endothelial cell growth (claimed). The method may be
CC used for inhibiting angiogenesis in a patient. The angiogenesis is
CC associated with a disease other than a tumor that is associated with
CC neovascularization (e.g. diabetic neuropathy, retrolental fibroplasia,
CC trachoma, neovascular glaucoma, psoriasis, angiofibromas, immune
CC inflammation, atherosclerosis, excessive wound repair, retinal
CC neovascularization, macular degeneration, corneal graft rejection,
CC contact lens overwear, Crohn's disease, non-immune inflammation,
CC rheumatoid arthritis, systemic lupus erythematosus, thyroiditis,
CC Goodpasture's syndrome, systemic vasculitis, scleroderma, Sjorgen's
CC syndrome, sarcoidosis and primary biliary cirrhosis). The method may
CC also be used for treating/inhibiting tumor growth especially
CC Kaposi's sarcoma (claimed).
XX
SQ Sequence 417 AA;

Query Match 100.0%; Score 180; DB 21; Length 417;
Best Local Similarity 100.0%; Pred. No. 4.2e-187;
Matches 180; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EPAYVFEQFLDGDGWTSRWIESKHKSDFKFLVSSGKFGYDDEKDKGLQTSQDARYAL 60
DB 18 epavyfkeqfldgdgwtswieskhksdfkflvssgkfygdeekdkglqtsqdarfyal 77
QY 61 SASPEPFSNGKGTLLVQFTVKHEQNIDCGGYVKLFPNSLDQTDHMGDSEYNIMFGPDIC 120
|||||

Db 19 RWIESKHKSDFKFLVSSGKFGYDDEKDKGLQTSQDARFYALSASFPSNKGOTLVVQF 78
DB 36 rwieskhksdfkflvssgkfygdeekdkglqtsqdarfyalasfepnsknqglvqvqf 95
QY 79 TVRHEQNIIDCGGYVKLFPNSLDQTDHMGDSEYNIMFGPDICGPGTKKVVHVFYKGNV 138
DB 96 tvkhequidcgggyvklfpnsldqtdmhgdseynimfgpdicgpgtkkvvhvfykgnv 155
|||||

Db 78 sasfepfsnkgqtlvvqftvkheqnidcgggyvklfpnsldqtdmhgdseynimfgpdic 137
QY 121 GPGTKKVVHVFYKGNVLIINKDIRCKDDETHLYTLIVRPDNTYEVKIDNSQVSGSLE 180
|||||
DB 138 gpgtkkvhvfnykgnvliinkdirckddefthlytlivrpdyevkldnsqvsagsle 197
|||||

RESULT 5
AAY00927
ID AAY00927 standard; Protein; 417 AA.
XX
AC AAY00927;
XX
DT 28-MAY-1999 (first entry)
XX
DE Calreticulin.
XX
KW Clq and collectin receptor; cClqR binding domain; complement ubiquitin;
KW CUB functionality; inhibitor; complement activation; inflammation;
KW myocardial infarction; brain ischaemia; gut ischaemia; amyloid plaque;
KW rheumatoid arthritis; systemic lupus erythematosus; Alzheimer's disease;
KW immune complex nephritis; therapy.
XX
OS Homo sapiens.
XX
PN WO9907406-A1.
XX
PD 18-FEB-1999.
XX
PF 12-AUG-1998; 98WO-GB02430.
XX
PR 12-AUG-1997; 97GB-0016998.
XX
PA (UYLE-) UNIV LEICESTER.
XX
PI Schwaeble W;
XX
DR WPI; 1999-180404/15.
XX
PT Use of a cClqR binding domain - to modulate complement ubiquitin
PT (CUB) functionality.
XX
PS Disclosure; Page 26-27; 31pp; English.
XX
CC This sequence is calreticulin, a homologue of Clq and collectin receptor
CC (cClqR). The invention relates to the use of a cClqR binding domain in a
CC medicament to effect complement ubiquitin (CUB) functionality, and an
CC inhibitor of the cClqR binding domain in a medicament to inhibit CUB
CC functionality. The cClqR binding domain, or its inhibitor, can be used to
CC treat a human or animal body. Particularly an inhibitor is used to treat
CC complement activation involved in the initiation and maintenance of
CC inflammation, for example in myocardial infarction, brain ischaemia
CC (stroke), gut ischaemia, rheumatoid arthritis, systemic lupus
CC erythematosus, burns, immune complex nephritis, and to treat amyloid
CC plaques in Alzheimer's disease. The use of cClqR binding domain or
CC inhibitor enables the CUB domain functionality to be modulated using a
CC low molecular weight molecule.
XX
SQ Sequence 417 AA;

Query Match 90.0%; Score 162; DB 20; Length 417;
Best Local Similarity 100.0%; Pred. No. 1.5e-167;
Matches 162; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 19 RWIESKHKSDFKFLVSSGKFGYDDEKDKGLQTSQDARFYALSASFPSNKGOTLVVQF 78
DB 36 rwieskhksdfkflvssgkfygdeekdkglqtsqdarfyalasfepnsknqglvqvqf 95
QY 79 TVRHEQNIIDCGGYVKLFPNSLDQTDHMGDSEYNIMFGPDICGPGTKKVVHVFYKGNV 138
DB 96 tvkhequidcgggyvklfpnsldqtdmhgdseynimfgpdicgpgtkkvvhvfykgnv 155
|||||
```

QY 139 LINKTRCKDDETHYTLIVRPDNTYEVKIDNSQVESGSL 180  
 Db 156 linkdirckddefthlytlivrpdpntyevkidnsqvesgsl 197

## RESULT 6

AAW11156  
 ID AAW11156 standard; peptide; 401 AA.  
 XX  
 AC AAW11156;  
 XX  
 DT 31-MAY-1997 (first entry)  
 XX  
 DE Calreticulin.  
 XX  
 KW calreticulin; C-domain; restenosis; inhibitor.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO9636643-A1.  
 XX  
 PD 21-NOV-1996.  
 XX  
 PF 17-MAY-1996; 96WO-IB00471.  
 XX  
 PR 16-MAY-1996; 96US-0649417.  
 PR 17-MAY-1995; 95US-0442844.  
 XX  
 PA (UYAL-) UNIV ALBERTA.  
 XX  
 PI Lucas A, Michalak M;  
 XX  
 DR WPI; 1997-012036/01.  
 XX  
 PT Inhibition of restenosis in patients - using calreticulin or a  
 PT C-domain polypeptide of calreticulin or a variant with the same  
 PT activity.  
 XX  
 PS Disclosure; Fig 1; 48pp; English.  
 XX  
 CC The present sequence is calreticulin. It and a C-domain derived peptide  
 CC (AAW06736) are useful for treating a patient to inhibit restenosis. The  
 CC calreticulin-type cpds. are administered either parenterally,  
 CC intravenously or via a catheter and can target areas of vascular damage  
 CC to inhibit or prevent restenosis.  
 XX  
 SQ Sequence 401 AA;

Query Match 42.8%; Score 77; DB 18; Length 401;  
 Best Local Similarity 100.0%; Pred. No. 3.1e-75;  
 Matches 77; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 104 DMHGDEYNIMFGPDICGPGTKKHVIFNYKGNVLINKDIRCKDDEFTHLYTLIVRPDN 163  
 Db 104 dmhgdeynimfgpdicgpgtkkhvifnykgnvlinkdirckddefthlytlivrpdn 163  
 QY 164 TYEVKIDNSQVESGSL 180  
 Db 164 tyevkidnsqvesgsl 180

## RESULT 7

AAAY92352  
 ID AAY92352 standard; Protein; 61 AA.  
 XX  
 AC AAY92352;  
 XX  
 DT 10-AUG-2000 (first entry)  
 XX  
 DE Recombinant human calreticulin residues 120-180.  
 XX  
 KW MBP-calreticulin; maltose binding protein; angiogenesis; inhibition;

KW endothelial cell; anti-angiogenic; neuroprotective; antidiabetic;  
 KW cytostatic; dermatologic; immunosuppressive; antiinflammatory; hepatic;  
 KW anti-atherosclerotic; gastrointestinal; anti-arthritis; ophthalmic.  
 XX  
 OS Homo sapiens.  
 OS Synthetic.  
 XX  
 PN WO200020577-A1.  
 XX  
 PD 13-APR-2000.  
 XX  
 PF 05-OCT-1999; 99WO-US23240.  
 XX  
 PR 06-OCT-1998; 98US-0103438.  
 XX  
 PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.  
 XX  
 PI Tosato G, Pike SE, Yao L;  
 XX  
 DR WPI; 2000-303767/26.  
 XX  
 PT Inhibiting endothelial cell growth and angiogenesis using calreticulin,  
 PT useful for suppressing tumor growth  
 XX  
 PS Claim 4; Page 82-83; 99pp; English.  
 XX  
 CC A novel method of inhibiting endothelial cell growth comprises  
 CC contacting the cells with calreticulin (or its fragments/variants).  
 CC Fragments of calreticulin causes at least 40% inhibition of angiogenesis,  
 CC tumor growth and/or endothelial cell growth (claimed). The method may be  
 CC used for inhibiting angiogenesis in a patient. The angiogenesis is  
 CC associated with a disease other than a tumor that is associated with  
 CC neovascularization (e.g. diabetic neuropathy, retrolental fibroplasia,  
 CC trachoma, neovascular glaucoma, psoriasis, angiodermas, immune  
 CC inflammation, atherosclerosis, excessive wound repair, retinal  
 CC neovascularization, macular degeneration, corneal graft rejection,  
 CC contact lens overwear, Crohn's disease, non-immune inflammation,  
 CC rheumatoid arthritis, systemic lupus erythematosus, thyroiditis,  
 CC Goodpasture's syndrome, systemic vasculitis, scleroderma, Sjorgen's  
 CC syndrome, sarcoidosis and primary biliary cirrhosis). The method may  
 CC also be used for treating/inhibiting tumor growth especially  
 CC Kaposi's sarcoma (claimed).  
 XX  
 SQ Sequence 61 AA;

Query Match 33.9%; Score 61; DB 21; Length 61;  
 Best Local Similarity 100.0%; Pred. No. 1.4e-58;  
 Matches 61; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 120 CGPGRKKVHVIFNYKGNVLINKDIRCKDDEFTHLYTLIVRPDNTYEVKIDNSQVESGSL 179  
 Db 1 cpgpgrkkvifnykgnvlinkdirckddefthlytlivrpdpntyevkidnsqvesgsl 60  
 QY 180 E 180  
 Db 61 e 61

## RESULT 8

AAAY92354  
 ID AAY92354 standard; Protein; 60 AA.  
 XX  
 AC AAY92354;  
 XX  
 DT 10-AUG-2000 (first entry)  
 XX  
 DE Recombinant human calreticulin residues 121-180.

KW MBP-calreticulin; maltose binding protein; angiogenesis; inhibition;  
 KW endothelial cell; anti-angiogenic; neuroprotective; antidiabetic;  
 KW cytostatic; dermatologic; immunosuppressive; antiinflammatory; hepatic;  
 KW anti-atherosclerotic; gastrointestinal; anti-arthritis; ophthalmic.

```

XX OS Homo sapiens.
XX OS Synthetic.
XX PN WO200020577-A1.
XX PN 13-APR-2000.
XX PF 05-OCT-1999; 99WO-US23240.
XX PR 06-OCT-1998; 98US-0103438.
XX PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX PI Tosato G, Pike SE, Yao L;
XX DR WPI; 2000-303767/26.
XX PT Inhibiting endothelial cell growth and angiogenesis using calreticulin,
XX PT useful for suppressing tumor growth
XX PS Claim 4; Page 85; 99pp; English.
XX CC A novel method of inhibiting endothelial cell growth comprises
XX CC contacting the cells with calreticulin (or its fragments/variants).
XX CC Fragments of calreticulin causes at least 40% inhibition of angiogenesis,
XX CC tumor growth and/or endothelial cell growth (claimed). The method may be
XX CC used for inhibiting angiogenesis in a patient. The angiogenesis is
XX CC associated with a disease other than a tumor that is associated with
XX CC neovascularization (e.g. diabetic neuropathy, retrolental fibroplasia,
XX CC trachoma, neovascular glaucoma, psoriasis, angiofibromas, immune
XX CC inflammation, atherosclerosis, excessive wound repair, retinal
XX CC neovascularization, macular degeneration, corneal graft rejection,
XX CC contact lens overwear, Crohn's disease, non-immune inflammation,
XX CC rheumatoid arthritis, systemic lupus erythromatosus, thyroiditis,
XX CC Goodpasture's syndrome, systemic vasculitis, scleroderma, Sjorgen's
XX CC syndrome, sarcoidosis and primary biliary cirrhosis). The method may
XX CC also be used for treating/inhibiting tumor growth especially
XX CC Kaposi's sarcoma (claimed).
XX SQ Sequence 60 AA;

Query Match 33.3%; Score 60; DB 21; Length 60;
Best Local Similarity 100.0%; Pred. No. 1.6e-57;
Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 121 GPGTKKHVIFNYKGNVLINKDKRDEFTHLTYTLIVRPDNTYEVKIDNSQVSGSLE 180
Db 1 gpgtkkhvifnykgnvlinkdkrcddefthlytlivrpdttyevkldnsqvsge 60

RESULT 9
AA92335
ID AAY92355 standard; Protein; 280 AA.
XX AC AAY92355;
XX DT 10-AUG-2000 (first entry)
XX DE Recombinant delta-120 calreticulin.
XX KW MBP-calreticulin; maltose binding protein; angiogenesis; inhibition;
XX KW endothelial cell; anti-angiogenic; neuroprotective; antidiabetic;
XX KW cytosolic; dermalogical; immunosuppressive; antiinflammatory; hepatic;
XX KW anti-atherosclerotic; gastrointestinal; anti-arthritis; ophthalmic.
XX OS Homo sapiens.
XX OS Synthetic.
XX PN WO200020577-A1.
XX PD 13-APR-2000.

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XX PF 05-OCT-1999; 99WO-US23240.
XX PR 06-OCT-1998; 98US-0103438.
XX PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX PI Tosato G, Pike SE, Yao L;
XX DR WPI; 2000-303767/26.
XX PT Inhibiting endothelial cell growth and angiogenesis using calreticulin,
XX PT useful for suppressing tumor growth
XX PS Claim 4; Page 86; 99pp; English.
XX CC This sequence comprises recombinant human calreticulin (AAY92350)
XX CC missing the N-terminal 120 amino acids.
XX CC A novel method of inhibiting endothelial cell growth comprises
XX CC contacting the cells with calreticulin (or its fragments/variants).
XX CC Fragments of calreticulin causes at least 40% inhibition of
XX CC angiogenesis, tumor growth and/or endothelial cell growth (claimed). The
XX CC method may be used for inhibiting angiogenesis in a patient. The
XX CC angiogenesis is associated with a disease other than a tumor that is
XX CC associated with neovascularization (e.g. diabetic neuropathy, retrolental
XX CC fibroplasia, trachoma, neovascular glaucoma, psoriasis, angiofibromas,
XX CC immune inflammation, atherosclerosis, excessive wound repair, retinal
XX CC neovascularization, macular degeneration, corneal graft rejection,
XX CC contact lens overwear, Crohn's disease, non-immune inflammation,
XX CC rheumatoid arthritis, systemic lupus erythromatosus, thyroiditis,
XX CC Goodpasture's syndrome, systemic vasculitis, scleroderma, Sjorgen's
XX CC syndrome, sarcoidosis and primary biliary cirrhosis). The method may
XX CC also be used for treating/inhibiting tumor growth especially
XX CC Kaposi's sarcoma (claimed).
XX SQ Sequence 280 AA;

Query Match 33.3%; Score 60; DB 21; Length 280;
Best Local Similarity 100.0%; Pred. No. 6.5e-57;
Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 121 GPGTKKHVIFNYKGNVLINKDKRDEFTHLTYTLIVRPDNTYEVKIDNSQVSGSLE 180
Db 1 gpgtkkhvifnykgnvlinkdkrcddefthlytlivrpdttyevkldnsqvsge 60

RESULT 10
AA92353
ID AAY92353 standard; Protein; 49 AA.
XX AC AAY92353;
XX DT 10-AUG-2000 (first entry)
XX DE Recombinant human calreticulin residues 132-180.
XX KW MBP-calreticulin; maltose binding protein; angiogenesis; inhibition;
XX KW endothelial cell; anti-angiogenic; neuroprotective; antidiabetic;
XX KW cytosolic; dermalogical; immunosuppressive; antiinflammatory; hepatic;
XX KW anti-atherosclerotic; gastrointestinal; anti-arthritis; ophthalmic.
XX OS Homo sapiens.
XX OS Synthetic.
XX PN WO200020577-A1.
XX PD 13-APR-2000.
XX PF 05-OCT-1999; 99WO-US23240.
XX PR 06-OCT-1998; 98US-0103438.
XX

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PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.

PI Tosato G, Pike SE, Yao L;

DR WPI; 2000-303767/26.

XX Inhibiting endothelial cell growth and angiogenesis using calreticulin,  
PT useful for suppressing tumor growth

XX Claim 4; Page 82-83; 99pp; English.

XX A novel method of inhibiting endothelial cell growth comprises  
CC contacting the cells with calreticulin (or its fragments/variants).  
CC Fragments of calreticulin causes at least 40% inhibition of angiogenesis,  
CC tumor growth and/or endothelial cell growth (claimed). The method may be  
CC used for inhibiting angiogenesis in a patient. The angiogenesis is  
CC associated with a disease other than a tumor that is associated with  
CC neovascularization (e.g. diabetic neuropathy, retrolental fibroplasia,  
CC trachoma, neovascular glaucoma, psoriasis, angiofibromas, immune  
CC inflammation, atherosclerosis, excessive wound repair, retinal  
CC neovascularization, macular degeneration, corneal graft rejection,  
CC contact lens overwear, Crohn's disease, non-immune inflammation,  
CC rheumatoid arthritis, systemic lupus erythematosus, thyroiditis,  
CC Goodpasture's syndrome, systemic vasculitis, scleroderma, Sjorgen's  
CC syndrome, sarcoidosis and primary biliary cirrhosis). The method may  
CC also be used for treating/inhibiting tumor growth especially  
CC Kaposi's sarcoma (claimed).

XX Sequence 49 AA;

Query Match 27.2%; Score 49; DB 21; Length 49;

Best Local Similarity 100.0%; Pred. No. 1.2e-45;

Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 132 NYKGNVLINKDICKDEFTHLYTLVRPDNTYEVKIDNSQVSGSLE 180

DB 1 nykgknvlindickdefthlytlvrpdntyevkidnsqvsgele 49

RESULT 11

AAAY00924

ID AAY00924 standard; Protein; 122 AA.

XX AAY00924;

DT 28-MAY-1999 (first entry)

DE Human cClqR binding domain protein sequence.

XX Clq and collectin receptor; cClqR binding domain; complement ubiquitin;  
KW CUB functionality; inhibitor; complement activation; inflammation;  
KW myocardial infarction; brain ischaemia; gut ischaemia; amyloid plaque;  
KW rheumatoid arthritis; systemic lupus erythematosus; Alzheimer's disease;  
KW immune complex nephritis; therapy.

OS Homo sapiens.

XX WO9907406-A1.

XX 18-FEB-1999.

XX 12-AUG-1998; 98WO-GB02430.

XX 12-AUG-1997; 97GB-0016998.

XX (UYLE-) UNIV LEICESTER.

XX Schwaeble W;

XX WPI; 1999-180404/15.

XX N-PSDB; AAX27251.

XX

PT Use of a cClqR binding domain - to modulate complement ubiquitin  
(CUB) functionality.

XX Claim 9; Page 23; 31pp; English.

XX This sequence is a Clq and collectin receptor (cClqR) binding  
CC domain. The invention relates to the use of a cClqR binding domain in a  
CC medicament to effect complement ubiquitin (CUB) functionality, and an  
CC inhibitor of the cClqR binding domain in a medicament to inhibit CUB  
CC functionality. The cClqR binding domain, or its inhibitor, can be used to  
CC treat a human or animal body. Particularly an inhibitor is used to treat  
CC complement activation involved in the initiation and maintenance of  
CC inflammation, for example in myocardial infarction, brain ischaemia  
CC (stroke), gut ischaemia, rheumatoid arthritis, systemic lupus  
CC erythematosus, burns, immune complex nephritis, and to treat amyloid  
CC plaques in Alzheimer's disease. The use of cClqR binding domain or  
CC inhibitor enables the CUB domain functionality to be modulated using a  
CC low molecular weight molecule.

XX Sequence 122 AA;

Query Match 20.0%; Score 36; DB 20; Length 122;

Best Local Similarity 100.0%; Pred. No. 3.6e-31;

Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 145 RCKDDEFTHLYTLVRPDNTYEVKIDNSQVSGSLE 180

DB 1 rckddefthlytlvrpdntyevkidnsqvsgele 36

RESULT 12

AAAY00926

ID AAY00926 standard; Protein; 122 AA.

XX AAY00926;

DT 28-MAY-1999 (first entry)

DE Rat cClqR binding domain protein sequence.

XX Clq and collectin receptor; cClqR binding domain; complement ubiquitin;  
KW CUB functionality; inhibitor; complement activation; inflammation;  
KW myocardial infarction; brain ischaemia; gut ischaemia; amyloid plaque;  
KW rheumatoid arthritis; systemic lupus erythematosus; Alzheimer's disease;  
KW immune complex nephritis; therapy.

OS Rattus norvegicus.

XX WO9907406-A1.

XX 18-FEB-1999.

XX 12-AUG-1998; 98WO-GB02430.

XX 12-AUG-1997; 97GB-0016998.

XX (UYLE-) UNIV LEICESTER.

XX Schwaeble W;

XX WPI; 1999-180404/15.

XX N-PSDB; AAX27253.

XX Use of a cClqR binding domain - to modulate complement ubiquitin  
(CUB) functionality.

XX Claim 9; Page 24-25; 31pp; English.

XX This sequence is a Clq and collectin receptor (cClqR) binding  
CC domain. The invention relates to the use of a cClqR binding domain in a  
CC medicament to effect complement ubiquitin (CUB) functionality, and an  
CC inhibitor of the cClqR binding domain in a medicament to inhibit CUB

CC functionality. The cClqR binding domain, or its inhibitor, can be used to  
 CC treat a human or animal body. Particularly an inhibitor is used to treat  
 CC complement activation involved in the initiation and maintenance of  
 CC inflammation, for example in myocardial infarction, brain ischaemia  
 CC (stroke), gut ischaemia, rheumatoid arthritis, systemic lupus  
 CC erythematosus, burns, immune complex nephritis, and to treat amyloid  
 CC plaques in Alzheimer's disease. The use of cClqR binding domain or  
 CC inhibitor enables the CUB domain functionality to be modulated using a  
 CC low molecular weight molecule.  
 XX  
 SQ Sequence 122 AA;

Query Match 20.0%; Score 36; DB 20; Length 122;  
 Best Local Similarity 100.0%; Pred. No. 3.6e-31;  
 Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 145 RCKDDETHLYTLIVRPDNTYEVKIDNSQVESGSL 180  
 |||||  
 Db 1 rckddefthlytlivrpdttyevkidnsqvesgsl 36

RESULT 13  
 AAY00925  
 ID AAY00925 standard; Protein; 122 AA.  
 AC AAY00925;  
 XX  
 XX 28-MAY-1999 (first entry)  
 DT  
 DE Mouse cClqR binding domain protein sequence.  
 XX  
 KW Clq and collectin receptor; cClqR binding domain; complement ubiquitin;  
 KW CUB functionality; inhibitor; complement activation; inflammation;  
 KW myocardial infarction; brain ischaemia; gut ischaemia; amyloid plaque;  
 KW rheumatoid arthritis; systemic lupus erythematosus; Alzheimer's disease;  
 KW immune complex nephritis; therapy.  
 XX  
 OS Mus musculus.  
 PN WO9907406-A1.  
 PD 18-FEB-1999.  
 XX  
 XX 12-AUG-1998; 98WO-GB02430.  
 PF  
 XX 12-AUG-1997; 97GB-0016998.  
 PR  
 PA (UYLE-) UNIV LEICESTER.  
 XX  
 XX Schwaible W;  
 PI  
 XX WPI: 1999-180404/15.  
 DR N-PSDB; AAX27252.  
 XX

PT Use of a cClqR binding domain - to modulate complement ubiquitin  
 PT (CUB) functionality.  
 XX  
 PS Claim 9; Page 24; 31pp; English.

CC This sequence is a Clq and collectin receptor (cClqR) binding  
 CC domain. The invention relates to the use of a cClqR binding domain in a  
 CC medicament to effect complement ubiquitin (CUB) functionality, and an  
 CC inhibitor of the cClqR binding domain in a medicament to inhibit CUB  
 CC functionality. The cClqR binding domain, or its inhibitor, can be used to  
 CC treat a human or animal body. Particularly an inhibitor is used to treat  
 CC complement activation involved in the initiation and maintenance of  
 CC inflammation, for example in myocardial infarction, brain ischaemia  
 CC (stroke), gut ischaemia, rheumatoid arthritis, systemic lupus  
 CC erythematosus, burns, immune complex nephritis, and to treat amyloid  
 CC plaques in Alzheimer's disease. The use of cClqR binding domain or  
 CC inhibitor enables the CUB domain functionality to be modulated using a  
 CC low molecular weight molecule.

XX  
 SQ Sequence 122 AA;

Query Match 10.6%; Score 19; DB 20; Length 122;  
 Best Local Similarity 100.0%; Pred. No. 1.1e-12;  
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 162 DNTYEVKIDNSQVESGSL 180  
 |||||  
 Db 18 dntyevkidnsqvesgsl 36

RESULT 14  
 AAR12312  
 ID AAR12312 standard; Protein; 336 AA.  
 XX  
 AC AAR12312;  
 XX  
 XX 29-AUG-1991 (first entry)  
 DT  
 DE Partial sequence of Onchocera volvulus 42 kD antigen.  
 XX  
 KW River blindness; onchocerciasis; vaccine; antigen; parasite.  
 XX  
 OS Onchocerca volvulus.  
 FH Key Location/Qualifiers  
 FT Region 160..166  
 FT /label= repeat unit  
 FT /note= "hydrophilic"  
 FT 177..183  
 FT Region  
 FT /label= repeat unit  
 FT /note= "hydrophilic"  
 FT 195..201  
 FT Region  
 FT /label= repeat unit  
 FT /note= "hydrophilic"

XX US5021342-A.  
 XX  
 XX 04-JUN-1991.  
 PD  
 XX 30-JUN-1988; 88US-0214264.  
 PF  
 XX 30-JUN-1988; 88US-0214264.  
 PR  
 XX (UYHO-) UNIV HOSPITALS CLEV.  
 PA  
 XX Greene BM, Unnasch TR;  
 PI  
 XX WPI: 1991-185179/25.  
 DR N-PSDB; AAQ11987.  
 XX  
 XX DNA encoding Onchocerca volvulus antigen - used to express  
 PT recombinant antigen for vaccine against onchocerciasis or river  
 PT blindness.  
 XX  
 XX Disclosure; Fig 7; 20pp; English.

CC The sequence was deduced from a cDNA clone lambda RAL-1 prep'd.  
 CC from RNA isolated from nodules excised from patients infected  
 CC with O. volvulus. The N-terminal is incomplete, however Abs  
 CC which specifically bind to protein prep'd. from induced cultures  
 CC of lambda RAL-1 lysogens recognise a single polypeptide of mol.  
 CC wt. 42,000 in extracts of adult worms. Analysis deduced sequence  
 CC suggests that it encodes a protein of mol. wt. 39,130. If the  
 CC antigen is not subject to post-translational processing this  
 CC suggests that most of the coding sequence is present. The three  
 CC repeats are highly hydrophilic regions likely to be exposed on  
 CC the surface of the antigen and highly immunogenic. Recombinant  
 CC antigen expressed by the clone can be used to stimulate T-cells of  
 CC individuals infected by the parasite to proliferate and may be  
 CC used as the basis for a vaccine against Onchocerciasis or river

CC blindness.

XX

SQ Sequence 336 AA;

Query Match 10.6%; Score 19; DB 12; Length 336;

Best Local Similarity 100.0%; Pred. No. 2.6e-12;

Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 113 IMRGPDICGGTKKVVHVF 131

|||||

Db 76 imrgpdicgpgtkkvhvf 94

Search completed: January 14, 2002, 08:50:53

Job time: 124 sec



GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: January 9, 2002, 15:01:12 ; Search time 83.2 Seconds  
(without alignments)  
24.038 Million cell updates/sec

Title: US-09-828-000-5

Perfect score: 151

Sequence: 1 CGPGTKKHVIFNYKGNVLINKDIRC 27

Scoring table:

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Gapop 10.0 , Gapext 0.5

Searched: 522463 seqs, 74073290 residues

Total number of hits satisfying chosen parameters: 522463

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	151	100.0	61	21	AA192352
2	151	100.0	180	21	AA192351
3	151	100.0	400	21	AA192350
4	151	100.0	401	18	AA111156
5	151	100.0	417	10	AA192276
6	151	100.0	417	20	AA1900927
7	151	100.0	417	21	AA192349
8	142	94.0	60	21	AA192354
9	142	94.0	280	21	AA192355
10	139	92.1	403	17	AA1904171
11	121	80.1	336	12	AA192312
					Recombinant human
					Human vasostatin (
					Recombinant human
					Calreticulin. Hom
					60 kD Ro (Ro/SSA)
					Calreticulin. Hom
					Human MBP-calretic
					Recombinant human
					Recombinant delta-
					Flea calreticulin
					Partial sequence o

12	82	54.3	49	21	AA192353	Recombinant human
13	82	54.3	415	22	AA192352	Castor bean calret
14	82	54.3	415	22	AA192351	Castor bean calret
15	79	52.3	312	21	AA192350	Arabidopsis thalia
16	79	52.3	312	21	AA192349	Arabidopsis thalia
17	79	52.3	332	21	AA192348	Arabidopsis thalia
18	79	52.3	421	21	AA192347	Arabidopsis thalia
19	79	52.3	421	21	AA192346	Arabidopsis thalia
20	79	52.3	421	21	AA192345	Arabidopsis thalia
21	79	52.3	424	21	AA192344	Arabidopsis thalia
22	79	52.3	441	21	AA192343	Arabidopsis thalia
23	79	52.3	444	21	AA192342	Arabidopsis thalia
24	61	40.4	385	21	AA192341	Human secreted pro
25	54	35.8	284	21	AA192340	Streptococcus pneu
26	54	35.8	720	22	AA192339	Recombinant P. fur
27	54	35.8	720	22	AA192338	P. furiosus helica
28	51	33.8	848	21	AA192337	Human NCAM 140kD i
29	50	33.1	490	21	AA192336	Arabidopsis thalia
30	49	32.5	9	19	AA192335	Bacillus caldocolin
31	49	32.5	593	13	AA192334	Bacillus caldocolin
32	49	32.5	876	14	AA192333	B. stearothermophil
33	49	32.5	876	18	AA192332	Bacillus caldocolin
34	49	32.5	877	13	AA192331	Bacillus caldocolin
35	49	32.5	877	18	AA192330	Bacillus caldocolin
36	49	32.5	877	18	AA192329	Bacillus caldocolin
37	49	32.5	877	18	AA192328	Bacillus caldocolin
38	48	31.8	17	20	AA192327	Peptide Seq ID No:
39	48	31.8	17	20	AA192326	Cell adhesion reco
40	48	31.8	17	21	AA192325	N-CAM heparin bind
41	48	31.8	17	21	AA192324	Cell adhesion reco
42	47.5	31.5	213	22	AA192323	C glutamic prote
43	47	31.1	490	17	AA192322	Arabidopsis adenyl
44	47	31.1	490	17	AA192321	Arabidopsis adenyl
45	47	31.1	490	20	AA192320	Arabidopsis adenyl

#### ALIGNMENTS

RESULT 1

AA192352

ID AA192352 standard; Protein; 61 AA.

XX AC AA192352;

XX AC AA192352;

DT 10-AUG-2000 (first entry)

XX DT 10-AUG-2000 (first entry)

DE Recombinant human calreticulin residues 120-180.

XX MBP-calreticulin; maltose binding protein; angiogenesis; inhibition;  
XX endothelial cell; anti-angiogenic; neuroprotective; antidiabetic;  
KW cytosolic; dermalogical; immunosuppressive; antiinflammatory; hepatic;  
KW anti-atherosclerotic; gastrointestinal; anti-arthritis; ophthalmic.

OS Homo sapiens.

XX OS Homo sapiens.

PN WO200020577-A1.

XX WO200020577-A1.

PD 13-APR-2000.

XX 13-APR-2000.

PF 05-OCT-1999; 99WO-US23240.

XX 05-OCT-1999; 99WO-US23240.

PR 06-OCT-1998; 98US-0103438.

XX 06-OCT-1998; 98US-0103438.

PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.

XX (USSH ) US DEPT HEALTH & HUMAN SERVICES.

PI Tosato G, Pike SE, Yao L;

XX Tosato G, Pike SE, Yao L;

DR WPI; 2000-303767/26.

XX WPI; 2000-303767/26.

PT Inhibiting endothelial cell growth and angiogenesis using calreticulin,  
PT useful for suppressing tumor growth

XX Claim 4; Page 82-83; 99pp; English.  
 PS  
 CC A novel method of inhibiting endothelial cell growth comprises  
 CC contacting the cells with calreticulin (or its fragments/variants).  
 CC Fragments of calreticulin causes at least 40% inhibition of angiogenesis,  
 CC tumor growth and/or endothelial cell growth (claimed). The method may be  
 CC used for inhibiting angiogenesis in a patient. The angiogenesis is  
 CC associated with a disease other than a tumor that is associated with  
 CC neovascularization (e.g. diabetic neuropathy, retrolental fibroplasia,  
 CC trachoma, neovascular glaucoma, psoriasis, angiofibromas, immune  
 CC inflammation, atherosclerosis, excessive wound repair, retinal  
 CC neovascularization, macular degeneration, corneal graft rejection,  
 CC contact lens overwear, Crohn's disease, non-immune inflammation,  
 CC rheumatoid arthritis, systemic lupus erythematosus, thyroiditis,  
 CC Goodpasture's syndrome, systemic vasculitis, scleroderma, Sjorgen's  
 CC syndrome, sarcoidosis and primary biliary cirrhosis). The method may  
 CC also be used for treating/inhibiting tumor growth especially  
 CC Kaposi's sarcoma (claimed).  
 XX  
 SQ Sequence 61 AA;

Query Match 100.0%; Score 151; DB 21; Length 61;  
 Best Local Similarity 100.0%; Pred. No. 2.5e-16;  
 Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGPGTKKHVHIFNYGKGNVLINKDIRC 27  
 |||||  
 Db 1 cqpqtkkhvhiynykgknvlinkdirc 27

RESULT 2  
 AAY92351  
 ID AAY92351 standard; Protein; 180 AA.

XX AC AAY92351;  
 XX 10-AUG-2000 (first entry)  
 XX DE Human vasostatin (calreticulin N-terminal 180 amino acids).  
 XX MBP-calreticulin; maltose binding protein; vasostatin; N-terminal;  
 KW angiogenesis; inhibition; endothelial cell; anti-angiogenic;  
 KW neuroprotective; antidiabetic; cytostatic; dermatological; hepatic;  
 KW immunosuppressive; anti-inflammatory; anti-atherosclerotic;  
 KW gastrointestinal; anti-arthritis; ophthalmic.

XX OS Homo sapiens.  
 XX Synthetic.  
 XX WO2000020577-A1.  
 XX 13-APR-2000.  
 XX 05-OCT-1999; 99WO-US23240.  
 XX 06-OCT-1998; 98US-0103438.  
 XX (USSH ) US DEPT HEALTH & HUMAN SERVICES.

XX Tosato G, Pike SE, Yao L;  
 XX WPI; 2000-303767/26.  
 XX Inhibiting endothelial cell growth and angiogenesis using calreticulin,  
 XX useful for suppressing tumor growth  
 XX Claim 4; Page 82; 99pp; English.

XX A novel method of inhibiting endothelial cell growth comprises  
 CC contacting the cells with calreticulin (or its fragments/variants).  
 CC Fragments of calreticulin causes at least 40% inhibition of angiogenesis,  
 CC tumor growth and/or endothelial cell growth (claimed). The method may be  
 CC used for inhibiting angiogenesis in a patient. The angiogenesis is  
 CC associated with a disease other than a tumor that is associated with  
 CC neovascularization (e.g. diabetic neuropathy, retrolental fibroplasia,  
 CC trachoma, neovascular glaucoma, psoriasis, angiofibromas, immune  
 CC inflammation, atherosclerosis, excessive wound repair, retinal  
 CC neovascularization, macular degeneration, corneal graft rejection,  
 CC contact lens overwear, Crohn's disease, non-immune inflammation,  
 CC rheumatoid arthritis, systemic lupus erythematosus, thyroiditis,  
 CC Goodpasture's syndrome, systemic vasculitis, scleroderma, Sjorgen's  
 CC syndrome, sarcoidosis and primary biliary cirrhosis). The method may  
 CC also be used for treating/inhibiting tumor growth especially  
 CC Kaposi's sarcoma (claimed).  
 XX

CC tumor growth and/or endothelial cell growth (claimed). The method may be  
 CC used for inhibiting angiogenesis in a patient. The angiogenesis is  
 CC associated with a disease other than a tumor that is associated with  
 CC neovascularization (e.g. diabetic neuropathy, retrolental fibroplasia,  
 CC trachoma, neovascular glaucoma, psoriasis, angiofibromas, immune  
 CC inflammation, atherosclerosis, excessive wound repair, retinal  
 CC neovascularization, macular degeneration, corneal graft rejection,  
 CC contact lens overwear, Crohn's disease, non-immune inflammation,  
 CC rheumatoid arthritis, systemic lupus erythematosus, thyroiditis,  
 CC Goodpasture's syndrome, systemic vasculitis, scleroderma, Sjorgen's  
 CC syndrome, sarcoidosis and primary biliary cirrhosis). The method may  
 CC also be used for treating/inhibiting tumor growth especially  
 CC Kaposi's sarcoma (claimed).  
 XX

SQ Sequence 180 AA;

Query Match 100.0%; Score 151; DB 21; Length 180;  
 Best Local Similarity 100.0%; Pred. No. 9e-16;  
 Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGPGTKKHVHIFNYGKGNVLINKDIRC 27  
 |||||  
 Db 120 cqpqtkkhvhiynykgknvlinkdirc 146

RESULT 3  
 AAY92350  
 ID AAY92350 standard; Protein; 400 AA.

XX AC AAY92350;  
 XX 10-AUG-2000 (first entry)  
 XX DE Recombinant human MBP-calreticulin.  
 XX MBP-calreticulin; maltose binding protein; angiogenesis; inhibition;  
 KW endothelial cell; anti-angiogenic; neuroprotective; antidiabetic;  
 KW cytostatic; dermatological; immunosuppressive; anti-inflammatory; hepatic;  
 KW anti-atherosclerotic; gastrointestinal; anti-arthritis; ophthalmic.

XX OS Homo sapiens.  
 XX WO2000020577-A1.  
 XX 13-APR-2000.  
 XX 05-OCT-1999; 99WO-US23240.  
 XX 06-OCT-1998; 98US-0103438.  
 XX (USSH ) US DEPT HEALTH & HUMAN SERVICES.

XX Tosato G, Pike SE, Yao L;  
 XX WPI; 2000-303767/26.  
 XX N-PSDB; AAA09346, AAA09347.  
 XX Inhibiting endothelial cell growth and angiogenesis using calreticulin,  
 XX useful for suppressing tumor growth  
 XX Claim 4; Page 80-81; 99pp; English.

XX Recombinant human MBP-calreticulin comprises the sequence of human  
 CC calreticulin (see AAY92349) without the 17 N-terminal amino acids.  
 CC A novel method of inhibiting endothelial cell growth comprises  
 CC contacting the cells with calreticulin (or its fragments/variants).  
 CC Fragments of calreticulin causes at least 40% inhibition of  
 CC angiogenesis, tumor growth and/or endothelial cell growth (claimed). The  
 CC method may be used for inhibiting angiogenesis in a patient. The  
 CC angiogenesis is associated with a disease other than a tumor that is  
 CC associated with neovascularization (e.g. diabetic neuropathy, retrolental  
 CC fibroplasia, trachoma, neovascular glaucoma, psoriasis, angiofibromas,



PD 18-FEB-1999.  
 XX PF 12-AUG-1998; 98WO-GB02430.  
 XX PR 12-AUG-1997; 97CB-0016998.  
 XX PA (UYLE-) UNIV LEICESTER.  
 XX PI Schwaeble W;  
 XX DR WPI; 1999-180404/15.  
 XX PT Use of a cClqR binding domain - to modulate complement ubiquitin  
 PT (CUB) functionality.  
 XX PT Disclosure; Page 26-27; 31pp; English.  
 XX CC This sequence is calreticulin, a homologue of Clq and collectin receptor  
 CC (cClqR). The invention relates to the use of a cClqR binding domain in a  
 CC medicament to effect complement ubiquitin (CUB) functionality, and an  
 CC inhibitor of the cClqR binding domain in a medicament to inhibit CUB  
 CC functionality. The cClqR binding domain, or its inhibitor, can be used to  
 CC treat a human or animal body. Particularly an inhibitor is used to treat  
 CC complement activation involved in the initiation and maintenance of  
 CC inflammation, for example in myocardial infarction, brain ischaemia  
 CC (stroke), gut ischaemia, rheumatoid arthritis, systemic lupus  
 CC erythematosus, burns, immune complex nephritis, and to treat amyloid  
 CC plaques in Alzheimer's disease. The use of cClqR binding domain or  
 CC inhibitor enables the CUB domain functionality to be modulated using a  
 CC low molecular weight molecule.  
 XX SQ Sequence 417 AA;

Query Match 100.0%; Score 151; DB 20; Length 417;  
 Best Local Similarity 100.0%; Pred. No. 2.4e-15;  
 Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 CGPGTKKHVHVIENYKGNVLINKDIRC 27  
 DB 137 CGPGTKKHVHVIENYKGNVLINKDIRC 163

RESULT 7  
 AAY92349  
 ID AAY92349 standard; Protein; 417 AA.  
 XX AC AAY92349;  
 XX DT 10-AUG-2000 (first entry)  
 XX DE Human MHP-calreticulin.  
 XX KW MBP-calreticulin; maltose binding protein; angiogenesis; inhibition;  
 KW endothelial cell; anti-angiogenic; neuroprotective; antidiabetic;  
 KW cytostatic; dermatological; immunosuppressive; antiinflammatory; hepatic;  
 KW anti-atherosclerotic; gastrointestinal; anti-arthritis; ophthalmic.  
 XX OS Homo sapiens.  
 XX FH Key Location/Qualifiers  
 FT Peptide 1..17  
 FT /label.. signal\_peptide  
 FT Protein 18  
 FT /label.. mature\_protein  
 XX WO200020577-A1.  
 XX PN 13-APR-2000.  
 XX PP 05-OCT-1999; 99WO-US23240.  
 XX PR 06-OCT-1998; 98US-0103438.

XX (USSH ) US DEPT HEALTH & HUMAN SERVICES.  
 XX PI Tosato G, Pike SE, Yao L;  
 XX DR WPI; 2000-303767/26.  
 XX DR N-PSDB; AAA09346, AAA09347.  
 XX PT Inhibiting endothelial cell growth and angiogenesis using calreticulin,  
 PT useful for suppressing tumor growth  
 XX PS Disclosure; Page 79-80; 99pp; English.  
 XX CC A novel method of inhibiting endothelial cell growth comprises  
 CC contacting the cells with calreticulin (or its fragments/variants).  
 CC Fragments of calreticulin causes at least 40% inhibition of angiogenesis,  
 CC tumor growth and/or endothelial cell growth (claimed). The method may be  
 CC used for inhibiting angiogenesis in a patient. The angiogenesis is  
 CC associated with a disease other than a tumor that is associated with  
 CC neovascularization (e.g. diabetic neuropathy, retrolental fibroplasia,  
 CC trachoma, neovascular glaucoma, psoriasis, angiofibromas, immune  
 CC inflammation, atherosclerosis, excessive wound repair, retinal  
 CC neovascularization, macular degeneration, corneal graft rejection,  
 CC contact lens overwear, Crohn's disease, non-immune inflammation,  
 CC rheumatoid arthritis, systemic lupus erythematosus, thyroiditis,  
 CC Goodpasture's syndrome, systemic vasculitis, scleroderma, Sjorgen's  
 CC syndrome, sarcoidosis and primary biliary cirrhosis). The method may  
 CC also be used for treating/inhibiting tumor growth especially  
 CC Kaposi's sarcoma (claimed).  
 XX SQ Sequence 417 AA;  
 Query Match 100.0%; Score 151; DB 21; Length 417;  
 Best Local Similarity 100.0%; Pred. No. 2.4e-15;  
 Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 CGPGTKKHVHVIENYKGNVLINKDIRC 27  
 DB 137 CGPGTKKHVHVIENYKGNVLINKDIRC 163  
 RESULT 8  
 AAY92354  
 ID AAY92354 standard; Protein; 60 AA.  
 XX AC AAY92354;  
 XX DT 10-AUG-2000 (first entry)  
 XX DE Recombinant human calreticulin residues 121-180.  
 XX KW MBP-calreticulin; maltose binding protein; angiogenesis; inhibition;  
 KW endothelial cell; anti-angiogenic; neuroprotective; antidiabetic;  
 KW cytostatic; dermatological; immunosuppressive; antiinflammatory; hepatic;  
 KW anti-atherosclerotic; gastrointestinal; anti-arthritis; ophthalmic.  
 XX OS Homo sapiens.  
 XX OS Synthetic.  
 XX PN WO200020577-A1.  
 XX PD 13-APR-2000.  
 XX PF 05-OCT-1999; 99WO-US23240.  
 XX PR 06-OCT-1998; 98US-0103438.  
 XX PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.  
 XX PI Tosato G, Pike SE, Yao L;  
 XX DR WPI; 2000-303767/26.

XX Inhibiting endothelial cell growth and angiogenesis using calreticulin,  
 PT useful for suppressing tumor growth  
 XX Claim 4; Page 85; 99pp; English.  
 XX A novel method of inhibiting endothelial cell growth comprises  
 CC contacting the cells with calreticulin (or its fragments/variants).  
 CC Fragments of calreticulin causes at least 40% inhibition of angiogenesis,  
 CC tumor growth and/or endothelial cell growth (claimed). The method may be  
 CC used for inhibiting angiogenesis in a patient. The angiogenesis is  
 CC associated with a disease other than a tumor that is associated with  
 CC neovascularization (e.g. diabetic neuropathy, retrolental fibroplasia,  
 CC trachoma, neovascular glaucoma, psoriasis, angiofibromas, immune  
 CC inflammation, atherosclerosis, excessive wound repair, retinal  
 CC neovascularization, macular degeneration, corneal graft rejection,  
 CC contact lens overwear, Crohn's disease, non-immune inflammation,  
 CC rheumatoid arthritis, systemic lupus erythromatosus, thyroiditis,  
 CC Goodpasture's syndrome, systemic vasculitis, scleroderma, Sjorgen's  
 CC syndrome, sarcoidosis and primary biliary cirrhosis). The method may  
 CC also be used for treating/inhibiting tumor growth especially  
 CC Kaposi's sarcoma (claimed).  
 XX Sequence 60 AA;

Query Match 94.0%; Score 142; DB 21; Length 60;  
 Best Local Similarity 100.0%; Pred. No. 6.4e-15;  
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 GPGTKKHVIFNYKGNVLINKDIRC 27  
 Db 1 gpgtkkhvifnykgnvlinkdirc 26

RESULT 9  
 AAY92355  
 ID AAY92355 standard; Protein; 280 AA.  
 XX  
 AC AAY92355;  
 XX  
 DT 10-AUG-2000 (first entry)  
 XX  
 DE Recombinant delta-120 calreticulin.  
 XX  
 KW MBP-calreticulin; maltose binding protein; angiogenesis; inhibition;  
 KW endothelial cell; anti-angiogenic; neuroprotective; antidiabetic;  
 KW cytosatic; dermalogical; immunosuppressive; antiinflammatory; hepatic;  
 KW anti-atherosclerotic; gastrointestinal; anti-arthritis; ophthalmic.  
 XX  
 OS Homo sapiens.  
 OS Synthetic.  
 XX  
 PN WO200020577-AL.  
 XX  
 PD 13-APR-2000.  
 XX  
 PF 05-OCT-1999; 99WO-US23240.  
 XX  
 PR 06-OCT-1998; 98US-0103438.  
 XX  
 PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.  
 XX  
 PI Tosato G, Pike SE, Yao L;  
 XX  
 XX WPI; 2000-303767/26.  
 DR  
 XX Inhibiting endothelial cell growth and angiogenesis using calreticulin,  
 PT useful for suppressing tumor growth  
 XX Claim 4; Page 86; 99pp; English.  
 XX This sequence comprises recombinant human calreticulin (AAY92350)  
 CC

CC missing the N-terminal 120 amino acids.  
 CC A novel method of inhibiting endothelial cell growth comprises  
 CC contacting the cells with calreticulin (or its fragments/variants).  
 CC Fragments of calreticulin causes at least 40% inhibition of  
 CC angiogenesis, tumor growth and/or endothelial cell growth (claimed). The  
 CC method may be used for inhibiting angiogenesis in a patient. The  
 CC angiogenesis is associated with a disease other than a tumor that is  
 CC associated with neovascularization (e.g. diabetic neuropathy, retrolental  
 CC fibroplasia, trachoma, neovascular glaucoma, psoriasis, angiofibromas,  
 CC immune inflammation, atherosclerosis, excessive wound repair, retinal  
 CC neovascularization, macular degeneration, corneal graft rejection,  
 CC contact lens overwear, Crohn's disease, non-immune inflammation,  
 CC rheumatoid arthritis, systemic lupus erythromatosus, thyroiditis,  
 CC Goodpasture's syndrome, systemic vasculitis, scleroderma, Sjorgen's  
 CC syndrome, sarcoidosis and primary biliary cirrhosis). The method may  
 CC also be used for treating/inhibiting tumor growth especially  
 CC Kaposi's sarcoma (claimed).  
 XX Sequence 280 AA;

Query Match 94.0%; Score 142; DB 21; Length 280;  
 Best Local Similarity 100.0%; Pred. No. 3.9e-14;  
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 GPGTKKHVIFNYKGNVLINKDIRC 27  
 Db 1 gpgtkkhvifnykgnvlinkdirc 26

RESULT 10  
 AAW04171  
 ID AAW04171 standard; Protein; 403 AA.  
 XX  
 AC AAW04171;  
 XX  
 DT 12-DEC-1996 (first entry)  
 XX  
 DE Flea calreticulin PctCal403.  
 XX  
 KW Calreticulin; flea; haematophagous insect; allergic dermatitis;  
 KW vaccine; therapy; PctCal403.  
 XX  
 OS Ctenocephalides felis.  
 OS  
 PN WO9628469-AL.  
 XX  
 PD 19-SEP-1996.  
 XX  
 PF 08-MAR-1996; 96WO-US03133.  
 XX  
 PR 09-MAR-1995; 95US-0401509.  
 XX  
 PA (HESK-) HESKA CORP.  
 XX  
 PI Rushlow KE, Stiegler GL;  
 XX  
 DR WPI; 1996-442861/44.  
 DR N-PSDB; AAT39516;  
 DR N-PSDB; AAT39517.  
 XX  
 HAematophagous insect calreticulin protein - used to reduce insect  
 infestation and desensitise patients to allergic dermatitis  
 XX Claim 5; Page 68-69; 86pp; English.  
 XX  
 CC Flea calreticulin protein PctCal1589 (AAW04171) is a calcium-binding  
 CC protein found in the salivary glands of Ctenocephalides felis.  
 CC Its amino acid sequence was deduced from a cDNA clone (AAT39516)  
 CC obtd. from a salivary gland cDNA library. Recombinant PctCal1589  
 CC can be produced in host cells transformed with a vector carrying  
 CC calreticulin nucleic acids. Calreticulin alters the blood feeding  
 CC behaviour of haematophagous insects and can be administered to an



SQ Sequence 49 AA;

Query Match 54.3%; Score 82; DB 21; Length 49;  
Best Local Similarity 100.0%; Pred. No. 1.2e-05;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 NYKGNVLINKDIRC 27  
|||||  
Db 1 nykgknvlinkdirc 15

RESULT 13

AAB66341  
ID AAB66341 standard; Protein: 415 AA.

XX AC AAB66341;

DT 05-APR-2001 (first entry)

XX Castor bean calreticulin SEQ ID NO: 2.

DE Castor bean; calreticulin; calcium binding; er; endoplasmic reticulum;  
KW calnexin; promoter; resistance.

XX Ricinus communis.

XX US6171864-B1.

PD 09-JAN-2001.

PF 05-JUL-1996; 96US-0675816.

PR 05-JUL-1996; 96US-0675816.

XX (PTON-) PIONEER HI-BRED INT INC.

PI Coughlan SJ, Winfrey RJ;

XX WPI; 2001-122335/13.

DR N-PSDB; AAF29741, AAF29742.

XX New nucleic acid molecules encoding a calcium binding chaperone protein  
in endoplasmic reticulum, calreticulin, and calreticulin promoter  
sequences, useful for producing foreign gene products in plant cells

PS Claim 1; Fig 3; 45pp; English.

XX The present invention provides the protein and coding sequences for the  
castor bean calreticulin protein and the calreticulin promoter sequence.  
In addition, the castor bean calnexin protein, coding sequence and  
promoter are also described. Calreticulin and calnexin are calcium  
binding proteins found in the endoplasmic reticulum (er). The  
calreticulin promoter sequence can be used in vectors to promote the  
expression of foreign genes, particularly resistance genes, in plant  
cells.

XX Sequence 415 AA;

Query Match 54.3%; Score 82; DB 22; Length 415;  
Best Local Similarity 55.6%; Pred. No. 0.00015;  
Matches 15; Conservative 2; Mismatches 10; Indels 0; Gaps 0;

QY 1 CGPGTKKHVIFNYKGNVLINKDIRC 27  
||| |||||  
Db 138 cgystkvhailnyndtnhlikkevpc 164

RESULT 14

AAB66343  
ID AAB66343 standard; Protein: 415 AA.

XX

AC AAB66343;

XX 05-APR-2001 (first entry)

DE Castor bean calreticulin.

XX Castor bean; calreticulin; calcium binding; er; endoplasmic reticulum;  
KW calnexin; promoter; resistance.

XX Ricinus communis.

XX US6171864-B1.

PD 09-JAN-2001.

PF 05-JUL-1996; 96US-0675816.

PR 05-JUL-1996; 96US-0675816.

XX (PTON-) PIONEER HI-BRED INT INC.

XX Coughlan SJ, Winfrey RJ;

XX WPI; 2001-122335/13.

DR N-PSDB; AAF29755.

XX New nucleic acid molecules encoding a calcium binding chaperone protein  
in endoplasmic reticulum, calreticulin, and calreticulin promoter  
sequences, useful for producing foreign gene products in plant cells

PS Disclosure; Fig 1B; 45pp; English.

XX The present invention provides the protein and coding sequences for the  
castor bean calreticulin protein and the calreticulin promoter sequence.  
In addition, the castor bean calnexin protein, coding sequence and  
promoter are also described. Calreticulin and calnexin are calcium  
binding proteins found in the endoplasmic reticulum (er). The  
calreticulin promoter sequence can be used in vectors to promote the  
expression of foreign genes, particularly resistance genes, in plant  
cells.

XX Sequence 415 AA;

Query Match 54.3%; Score 82; DB 22; Length 415;  
Best Local Similarity 55.6%; Pred. No. 0.00015;  
Matches 15; Conservative 2; Mismatches 10; Indels 0; Gaps 0;

QY 1 CGPGTKKHVIFNYKGNVLINKDIRC 27  
||| |||||  
Db 138 cgystkvhailnyndtnhlikkevpc 164

RESULT 15

AAG24609

ID AAG24609 standard; Protein: 312 AA.

XX AC AAG24609;

XX 17-OCT-2000 (first entry)

DE Arabidopsis thaliana protein fragment SEQ ID NO: 28351.

XX Protein identification; signal transduction pathway; metabolic pathway;  
KW hybridisation assay; genetic mapping; gene expression control; promoter;  
termination sequence.

XX Arabidopsis thaliana.

XX EP1033405-A2.

XX 06-SEP-2000.

XX

PF 25-FEB-2000; 2000RP-0301439.  
XX  
25-FEB-1999; 99US-0121825.  
PR 05-MAR-1999; 99US-0123180.  
PR 09-MAR-1999; 99US-0123548.  
PR 23-MAR-1999; 99US-0125788.  
PR 25-MAR-1999; 99US-0126264.  
PR 29-MAR-1999; 99US-0126785.  
PR 01-APR-1999; 99US-0127462.  
PR 06-APR-1999; 99US-0128234.  
PR 08-APR-1999; 99US-0128714.  
PR 16-APR-1999; 99US-0129845.  
PR 19-APR-1999; 99US-0130077.  
PR 21-APR-1999; 99US-0130449.  
PR 23-APR-1999; 99US-0130510.  
PR 23-APR-1999; 99US-0130891.  
PR 28-APR-1999; 99US-0131449.  
PR 30-APR-1999; 99US-0132048.  
PR 30-APR-1999; 99US-0132407.  
PR 04-MAY-1999; 99US-0132484.  
PR 05-MAY-1999; 99US-0132485.  
PR 06-MAY-1999; 99US-0132486.  
PR 06-MAY-1999; 99US-0132487.  
PR 07-MAY-1999; 99US-0132863.  
PR 11-MAY-1999; 99US-0134256.  
PR 14-MAY-1999; 99US-0134218.  
PR 14-MAY-1999; 99US-0134219.  
PR 14-MAY-1999; 99US-0134221.  
PR 14-MAY-1999; 99US-0134370.  
PR 18-MAY-1999; 99US-0134768.  
PR 19-MAY-1999; 99US-0134941.  
PR 20-MAY-1999; 99US-0135124.  
PR 21-MAY-1999; 99US-0135353.  
PR 24-MAY-1999; 99US-0135629.  
PR 25-MAY-1999; 99US-0136021.  
PR 27-MAY-1999; 99US-0136392.  
PR 28-MAY-1999; 99US-0136782.  
PR 01-JUN-1999; 99US-0137222.  
PR 03-JUN-1999; 99US-0137528.  
PR 04-JUN-1999; 99US-0137502.  
PR 07-JUN-1999; 99US-0137724.  
PR 08-JUN-1999; 99US-0138094.  
PR 10-JUN-1999; 99US-0138540.  
PR 10-JUN-1999; 99US-0138847.  
PR 14-JUN-1999; 99US-0139119.  
PR 16-JUN-1999; 99US-0139452.  
PR 16-JUN-1999; 99US-0139453.  
PR 17-JUN-1999; 99US-0139492.  
PR 18-JUN-1999; 99US-0139454.  
PR 18-JUN-1999; 99US-0139455.  
PR 18-JUN-1999; 99US-0139456.  
PR 18-JUN-1999; 99US-0139457.  
PR 18-JUN-1999; 99US-0139458.  
PR 18-JUN-1999; 99US-0139459.  
PR 18-JUN-1999; 99US-0139460.  
PR 18-JUN-1999; 99US-0139461.  
PR 18-JUN-1999; 99US-0139462.  
PR 18-JUN-1999; 99US-0139463.  
PR 18-JUN-1999; 99US-0139750.  
PR 18-JUN-1999; 99US-0139763.  
PR 21-JUN-1999; 99US-0139817.  
PR 22-JUN-1999; 99US-0139899.  
PR 23-JUN-1999; 99US-0140353.  
PR 23-JUN-1999; 99US-0140354.  
PR 24-JUN-1999; 99US-0140695.  
PR 28-JUN-1999; 99US-0140823.  
PR 29-JUN-1999; 99US-0140991.  
PR 30-JUN-1999; 99US-0141287.  
PR 01-JUL-1999; 99US-0141842.  
PR 01-JUL-1999; 99US-0142154.  
PR 02-JUL-1999; 99US-0142055.  
PR 06-JUL-1999; 99US-0142390.  
PR 08-JUL-1999; 99US-0142803.

PR 09-JUL-1999; 99US-0142920.  
PR 12-JUL-1999; 99US-0142977.  
PR 13-JUL-1999; 99US-0143542.  
PR 14-JUL-1999; 99US-0143624.  
PR 15-JUL-1999; 99US-0144005.  
PR 16-JUL-1999; 99US-0144085.  
PR 16-JUL-1999; 99US-0144086.  
PR 19-JUL-1999; 99US-0144325.  
PR 19-JUL-1999; 99US-0144331.  
PR 19-JUL-1999; 99US-0144332.  
PR 19-JUL-1999; 99US-0144333.  
PR 19-JUL-1999; 99US-0144334.  
PR 19-JUL-1999; 99US-0144335.  
PR 20-JUL-1999; 99US-0144352.  
PR 20-JUL-1999; 99US-0144632.  
PR 20-JUL-1999; 99US-0144684.  
PR 21-JUL-1999; 99US-0144814.  
PR 21-JUL-1999; 99US-0145086.  
PR 21-JUL-1999; 99US-0145088.  
PR 22-JUL-1999; 99US-0145085.  
PR 22-JUL-1999; 99US-0145087.  
PR 22-JUL-1999; 99US-0145089.  
PR 22-JUL-1999; 99US-0145192.  
PR 23-JUL-1999; 99US-0145145.  
PR 23-JUL-1999; 99US-0145218.  
PR 23-JUL-1999; 99US-0145224.  
PR 26-JUL-1999; 99US-0145276.  
PR 27-JUL-1999; 99US-0145913.  
PR 27-JUL-1999; 99US-0145918.  
PR 27-JUL-1999; 99US-0145919.  
PR 28-JUL-1999; 99US-0145951.  
PR 02-AUG-1999; 99US-0146386.  
PR 02-AUG-1999; 99US-0146388.  
PR 03-AUG-1999; 99US-0146389.  
PR 03-AUG-1999; 99US-0147038.  
PR 04-AUG-1999; 99US-0147204.  
PR 04-AUG-1999; 99US-0147302.  
PR 05-AUG-1999; 99US-0147192.  
PR 05-AUG-1999; 99US-0147260.  
PR 06-AUG-1999; 99US-0147303.  
PR 06-AUG-1999; 99US-0147416.  
PR 09-AUG-1999; 99US-0147493.  
PR 09-AUG-1999; 99US-0147935.  
PR 10-AUG-1999; 99US-0148171.  
PR 11-AUG-1999; 99US-0148319.  
PR 12-AUG-1999; 99US-0148341.  
PR 13-AUG-1999; 99US-0148565.  
PR 13-AUG-1999; 99US-0148684.  
PR 16-AUG-1999; 99US-0149368.  
PR 17-AUG-1999; 99US-0149175.  
PR 18-AUG-1999; 99US-0149426.  
PR 20-AUG-1999; 99US-0149722.  
PR 20-AUG-1999; 99US-0149723.  
PR 20-AUG-1999; 99US-0149922.  
PR 23-AUG-1999; 99US-0149902.  
PR 23-AUG-1999; 99US-0149930.  
PR 25-AUG-1999; 99US-0150566.  
PR 26-AUG-1999; 99US-0150884.  
PR 27-AUG-1999; 99US-0151065.  
PR 27-AUG-1999; 99US-0151066.  
PR 27-AUG-1999; 99US-0151080.  
PR 30-AUG-1999; 99US-0151303.  
PR 31-AUG-1999; 99US-0151438.  
PR 01-SEP-1999; 99US-0151930.  
PR 07-SEP-1999; 99US-0152363.  
PR 10-SEP-1999; 99US-0153070.  
PR 13-SEP-1999; 99US-0153758.  
PR 15-SEP-1999; 99US-0154018.  
PR 16-SEP-1999; 99US-0154039.  
PR 20-SEP-1999; 99US-0154779.  
PR 22-SEP-1999; 99US-0155139.  
PR 23-SEP-1999; 99US-0155486.  
PR 24-SEP-1999; 99US-0155659.



PR	28-SEP-1999;	99US-0156458.
PR	29-SEP-1999;	99US-0156596.
PR	04-OCT-1999;	99US-0157117.
PR	05-OCT-1999;	99US-0157753.
PR	06-OCT-1999;	99US-0157865.
PR	07-OCT-1999;	99US-0158029.
PR	08-OCT-1999;	99US-0158232.
PR	12-OCT-1999;	99US-0158369.
PR	13-OCT-1999;	99US-0159293.
PR	13-OCT-1999;	99US-0159294.
PR	13-OCT-1999;	99US-0159295.
PR	14-OCT-1999;	99US-0159329.
PR	14-OCT-1999;	99US-0159330.
PR	14-OCT-1999;	99US-0159331.
PR	14-OCT-1999;	99US-0159637.
PR	14-OCT-1999;	99US-0159638.
PR	18-OCT-1999;	99US-0159584.
PR	21-OCT-1999;	99US-0160741.
PR	21-OCT-1999;	99US-0160767.
PR	21-OCT-1999;	99US-0160768.
PR	21-OCT-1999;	99US-0160770.
PR	21-OCT-1999;	99US-0160814.
PR	21-OCT-1999;	99US-0160815.
PR	22-OCT-1999;	99US-0160980.
PR	22-OCT-1999;	99US-0160981.
PR	22-OCT-1999;	99US-0160989.
PR	25-OCT-1999;	99US-0161404.
PR	25-OCT-1999;	99US-0161405.
PR	25-OCT-1999;	99US-0161406.
PR	26-OCT-1999;	99US-0161359.
PR	26-OCT-1999;	99US-0161360.
PR	26-OCT-1999;	99US-0161361.
PR	28-OCT-1999;	99US-0161920.
PR	28-OCT-1999;	99US-0161992.
PR	28-OCT-1999;	99US-0161993.
PR	29-OCT-1999;	99US-0162142.

Query Match 52.3%; Score 79; DB 21; Length 312;  
Best Local Similarity 55.6%; Pred. No. 0.00032;  
Matches 15; Conservative 1; Mismatches 11; Indels

Qy 1 CGPGTKKVHVIFNYKGKNVLINKDIRC 27  
 || ||||| | | | |||: |  
 Db 28 cgystkkvhaltyneanhlikkdvc 54

Search completed: January 9, 2002, 15:01:13  
Job time: 159 sec



GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: January 9, 2002, 14:58:34 ; Search time 83.2 Seconds  
(without alignments)  
160.255 Million cell updates/sec

Title: us-09-828-000-3  
Perfect score: 971  
Sequence: 1 EFAVYKEFLDGDGWTSRW.....PDNTYEVKIDNSOVESGSL E 180

Scoring table:  
BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 522463 seqs, 74073290 residues

Total number of hits satisfying chosen parameters: 522463

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A\_Geneseq\_1101.\*  
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20: /SID88/gcgdata/geneseq/geneseq/AA1999.DAT.\*  
21: /SID88/gcgdata/geneseq/geneseq/AA2000.DAT.\*  
22: /SID88/gcgdata/geneseq/geneseq/AA2001.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	971	100.0	180	21	AA192351 Human vasostatin (
2	971	100.0	400	21	AA192350 Recombinant human
3	971	100.0	417	10	AA192276 60 kD RO (Ro/SSA)
4	971	100.0	417	21	AA192349 Human MBP-calretic
5	966	99.5	417	20	AA1900927 Calreticulin. Hom
6	921	94.9	401	18	AA111156 Calreticulin. Hom
7	700	72.1	403	17	AA1904171 Flea calreticulin
8	631	65.0	385	21	AA192385 Human secreted pro
9	541.5	55.8	336	12	AA192312 Partial sequence o
10	527	54.3	415	22	AA1966341 Castor bean calret
11	527	54.3	415	22	AA1966343 Castor bean calret

12	510	52.5	421	21	AA1924608 Arabidopsis thalia
13	510	52.5	421	21	AA1924607 Arabidopsis thalia
14	510	52.5	424	21	AA1924607 Arabidopsis thalia
15	510	52.5	424	21	AA1924607 Arabidopsis thalia
16	510	52.5	441	21	AA1924607 Arabidopsis thalia
17	510	52.5	444	21	AA1924607 Arabidopsis thalia
18	327	33.7	61	21	AA192352 Recombinant human
19	318	32.7	60	21	AA192354 Recombinant human
20	318	32.7	280	21	AA192355 Recombinant delta-
21	301.5	31.1	417	21	AA192355 A. thaliana enviro
22	290	29.9	593	16	AA192355 Calnexin sequence.
23	258	26.6	49	21	AA192353 Recombinant human
24	253	26.1	312	21	AA1924609 Arabidopsis thalia
25	253	26.1	312	21	AA1924609 Arabidopsis thalia
26	253	26.1	332	21	AA1924609 Arabidopsis thalia
27	250.5	25.8	84	21	AA1924609 Arabidopsis thalia
28	238.5	24.6	530	21	AA1924609 Arabidopsis thalia
29	238.5	24.6	530	21	AA1924609 Arabidopsis thalia
30	238.5	24.6	567	21	AA1924609 Arabidopsis thalia
31	227.5	23.4	542	22	AA1924609 Arabidopsis thalia
32	200.5	20.6	532	21	AA1924609 Arabidopsis thalia
33	200.5	20.6	548	21	AA1924609 Arabidopsis thalia
34	190	19.6	122	20	AA1924609 Arabidopsis thalia
35	190	19.6	122	20	AA1924609 Arabidopsis thalia
36	182	18.7	122	20	AA1924609 Arabidopsis thalia
37	145	14.9	91	21	AA1924609 Arabidopsis thalia
38	145	14.9	99	21	AA1924609 Arabidopsis thalia
39	140.5	14.5	256	22	AA1924609 Arabidopsis thalia
40	124.5	12.8	221	21	AA1924609 Arabidopsis thalia
41	114.5	11.8	162	21	AA1924609 Arabidopsis thalia
42	114.5	11.8	162	21	AA1924609 Arabidopsis thalia
43	112.5	11.6	394	21	AA1924609 Arabidopsis thalia
44	112.5	11.6	394	21	AA1924609 Arabidopsis thalia
45	110.5	11.4	125	21	AA1924609 Arabidopsis thalia

#### ALIGNMENTS

RESULT 1  
AA192351  
ID AA192351 standard; Protein; 180 AA.  
AC AA192351;  
XX  
XX  
DT 10-AUG-2000 (first entry)  
XX  
DE Human vasostatin (calreticulin N-terminal 180 amino acids).  
XX  
KW MBP-calreticulin; maltose binding protein; vasostatin; N-terminal; angiogenesis; inhibition; endothelial cell; anti-angiogenic;  
KW neuroprotective; antidiabetic; cytostatic; dermatological; hepatic;  
KW immunosuppressive; anti-inflammatory; anti-atherosclerotic;  
KW gastrointestinal; anti-arthritis; ophthalmic.  
XX Homo sapiens.  
OS Synthetic.  
XX  
XX WO200020577-A1.  
PN  
XX  
PD 13-APR-2000.  
XX  
XX 05-OCT-1999; 99WO-US23240.  
XX  
XX 06-OCT-1998; 98US-0103438.  
XX  
XX (USSH ) US DEPT HEALTH & HUMAN SERVICES.  
XX  
XX Tosato G, Pike SE, Yao L;  
XX  
XX WPI; 2000-303767/26.  
XX  
XX Inhibiting endothelial cell growth and angiogenesis using calreticulin, PT

PT useful for suppressing tumor growth  
 PS Claim 4; Page 82; 99pp; English.

CC A novel method of inhibiting endothelial cell growth comprises  
 CC contacting the cells with calreticulin (or its fragments/variants).  
 CC Fragments of calreticulin causes at least 40% inhibition of angiogenesis,  
 CC tumor growth and/or endothelial cell growth (claimed). The method may be  
 CC used for inhibiting angiogenesis in a patient. The angiogenesis is  
 CC associated with a disease other than a tumor that is associated with  
 CC neovascularization (e.g. diabetic neuropathy, retrolental fibroplasia,  
 CC trachoma, neovascular glaucoma, psoriasis, angiofibromas, immune  
 CC inflammation, atherosclerosis, excessive wound repair, retinal  
 CC neovascularization, macular degeneration, corneal graft rejection,  
 CC contact lens overwear, Crohn's disease, non-immune inflammation,  
 CC rheumatoid arthritis, systemic lupus erythematosus, thyroiditis,  
 CC Goodpasture's syndrome, systemic vasculitis, scleroderma, Sjorgen's  
 CC syndrome, sarcoidosis and primary biliary cirrhosis). The method may  
 CC also be used for treating/inhibiting tumor growth especially  
 CC Kaposi's sarcoma (claimed).

XX Sequence 180 AA;

Query Match 100.0%; Score 971; DB 21; Length 180;  
 Best Local Similarity 100.0%; Pred. No. 3.1e-95;  
 Matchew 180; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PPAVYFKQFLDGDGWTSRWIESKHKSDPGKFLVSSGKFGYGDDEKDKGLQTSQDARFYAL 60  
 DB 1 PPAVYFKQFLDGDGWTSRWIESKHKSDPGKFLVSSGKFGYGDDEKDKGLQTSQDARFYAL 60  
 QY 61 SASFEPFNKGGOTLVVQFTVKHEQNDICGGYVVKLFPSLQDTMHGDSSEYNIMFGPDIC 120  
 DB 61 SASFEPFNKGGOTLVVQFTVKHEQNDICGGYVVKLFPSLQDTMHGDSSEYNIMFGPDIC 120  
 QY 121 GPGTKKHVIFNYKGNKVLINKDKDEFTHLTYTLVRPNTVEVKIDNSQVSGSLE 180  
 DB 121 GPGTKKHVIFNYKGNKVLINKDKDEFTHLTYTLVRPNTVEVKIDNSQVSGSLE 180

RESULT 2

AAY92350  
 ID AAY92350 standard; Protein; 400 AA.

XX AAY92350;

XX 10-AUG-2000 (first entry)

XX Recombinant human MBP-calreticulin.

XX MBP-calreticulin; maltose binding protein; angiogenesis; inhibition;  
 KW endothelial cell; anti-angiogenic; neuroprotective; antidiabetic;  
 KW cytotoxic; dermatologic; immunosuppressive; antiinflammatory; hepatic;  
 KW anti-atherosclerotic; gastrointestinal; anti-arthritis; ophthalmic.

OS Homo sapiens.

XX WO200020577-A1.

XX 13-APR-2000.

XX 05-OCT-1999; 99WO-US23240.

XX 06-OCT-1999; 98US-0103438.

XX (USSH ) US DEPT HEALTH & HUMAN SERVICES.

XX Tosato G, Pike SE, Yao L;

XX WPI; 2000-303767/26.

XX N-PSDB; AAA09346, AAA09347.

XX

PT Inhibiting endothelial cell growth and angiogenesis using calreticulin,  
 XX useful for suppressing tumor growth  
 PS Claim 4; Page 80-81; 99pp; English.

CC Recombinant human MBP-calreticulin comprises the sequence of human  
 CC calreticulin (see AAY92349) without the 17 N-terminal amino acids.  
 CC A novel method of inhibiting endothelial cell growth comprises  
 CC contacting the cells with calreticulin (or its fragments/variants).  
 CC Fragments of calreticulin causes at least 40% inhibition of  
 CC angiogenesis, tumor growth and/or endothelial cell growth (claimed). The  
 CC method may be used for inhibiting angiogenesis in a patient. The  
 CC angiogenesis is associated with a disease other than a tumor that is  
 CC associated with neovascularization (e.g. diabetic neuropathy, retrolental  
 CC fibroplasia, trachoma, neovascular glaucoma, psoriasis, angiofibromas,  
 CC immune inflammation, atherosclerosis, excessive wound repair, retinal  
 CC neovascularization, macular degeneration, corneal graft rejection,  
 CC contact lens overwear, Crohn's disease, non-immune inflammation,  
 CC rheumatoid arthritis, systemic lupus erythematosus, thyroiditis,  
 CC Goodpasture's syndrome, systemic vasculitis, scleroderma, Sjorgen's  
 CC syndrome, sarcoidosis and primary biliary cirrhosis). The method may  
 CC also be used for treating/inhibiting tumor growth especially  
 CC Kaposi's sarcoma (claimed).

XX Sequence 400 AA;

Query Match 100.0%; Score 971; DB 21; Length 400;  
 Best Local Similarity 100.0%; Pred. No. 9.4e-99;  
 Matches 180; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PPAVYFKQFLDGDGWTSRWIESKHKSDPGKFLVSSGKFGYGDDEKDKGLQTSQDARFYAL 60  
 DB 1 PPAVYFKQFLDGDGWTSRWIESKHKSDPGKFLVSSGKFGYGDDEKDKGLQTSQDARFYAL 60  
 QY 61 SASFEPFNKGGOTLVVQFTVKHEQNDICGGYVVKLFPSLQDTMHGDSSEYNIMFGPDIC 120  
 DB 61 SASFEPFNKGGOTLVVQFTVKHEQNDICGGYVVKLFPSLQDTMHGDSSEYNIMFGPDIC 120  
 QY 121 GPGTKKHVIFNYKGNKVLINKDKDEFTHLTYTLVRPNTVEVKIDNSQVSGSLE 180  
 DB 121 GPGTKKHVIFNYKGNKVLINKDKDEFTHLTYTLVRPNTVEVKIDNSQVSGSLE 180

RESULT 3

AAP92276  
 ID AAP92276 standard; protein; 417 AA.

XX AAP92276;

XX 23-FEB-1990 (first entry)

XX 60 kD Ro (Ro/SSA) antigen.

XX Sjorens syndrome; systemic lupus erythematosus.

OS Synthetic.

XX WO8909273-A.

XX 05-OCT-1989.

XX 22-MAR-1989; 89WO-US01213.

XX 22-MAR-1988; 88US-0171634.

XX (TEXA ) UNIV OF TEXAS SVST.

XX Sontheimer RD, Capra JD, McCauliffe DP;

XX WPI; 1989-309537/42.

XX N-PSDB; AAP92276.

XX

PT DNA sequences encoding antigenic epitope(s) of Ro 60 kD autoantigen  
XX - used in immunoassays to detect rheumatic disease  
PS Disclosure; Fig 2; 88pp; English.  
XX  
CC Synthetic peptides corresp. to an epitopic core of Ro antigen are  
CC expressed recombinantly to detect autoantibodies, for identification  
CC of autoimmune diseases. These epitopes are AAs 24-36, 23-36, 188-209,  
CC or 241-255. The peptides may be substd. for ribonucleoprotein particle  
XX antigens.  
XX  
SQ Sequence 417 AA;

Query Match 100.0%; Score 971; DB 10; Length 417;  
Best Local Similarity 100.0%; Pred. No. 9.9e-99;  
Matches 180; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 EPAVYFKEQFLDGDGWTSRWIESKHKSDFGKFLVSSGKFGYGDDEKDKGLQTSQDARFYAL 60  
Db 18 epavyfkeqfldgdgwtswieskhksdfgkflvssgkfygdeekdkglqtsqdarfyal 77  
Qy 61 SASFPFSSKNGQTLVVQFTVKHEQNTDCGGVYVKLFPSNLDQTMHGDSEYNMFPGDIC 120  
Db 78 sasfepfsnkgqtlvvqftvkheqnldcgggyvki f pnsldqtdm hgdseynm fgpdc 137  
Qy 121 GPGTKKVHVFYFNKGNVLINKDIRCKDDEFTHLYTLIVRPONTYEVKIDNSQVESGSLE 180  
Db 138 gpgtkkvhvfnykgnvlinkdirckddefthlytlivrpontyevkidnsqvesgsle 197

RESULT 4  
AAV92349  
ID AAV92349 standard; Protein; 417 AA.  
XX  
AC AAV92349;  
XX  
DT 10-AUG-2000 (first entry)  
XX  
DE Human MBP-calreticulin.

KW MBP-calreticulin; maltose binding protein; angiogenesis; inhibition;  
KW endothelial cell; anti-angiogenic; neuroprotective; antidiabetic;  
KW cytosatic; demagogical; immunosuppressive; antiinflammatory; hepatic;  
KW anti-atherosclerotic; gastrointestinal; anti-arthritis; ophthalmic.  
XX  
OS Homo sapiens.

FH Key Location/Qualifiers  
FT Peptide 1..17  
FT /label= signal\_peptide  
FT Protein 18  
FT /label= mature\_protein

XX WO200020577-A1.  
PN  
XX  
XX 13-APR-2000.  
XX  
XX 05-OCT-1999; 99WO-US23240.  
XX  
XX 06-OCT-1998; 98US-0103438.  
XX  
XX (USSH ) US DEPT HEALTH & HUMAN SERVICES.  
XX  
XX Tosato G, Pike SE, Yao L;  
XX WPI; 2000-303767/26.  
DR N-PSDB; AAA09346, AAA09347.  
XX  
XX Inhibiting endothelial cell growth and angiogenesis using calreticulin,  
PT useful for suppressing tumor growth  
PS Disclosure; Page 79-80; 99pp; English.

XX A novel method of inhibiting endothelial cell growth comprises  
CC contacting the cells with calreticulin (or its fragments/variants).  
CC Fragments of calreticulin causes at least 40% inhibition of angiogenesis,  
CC tumor growth and/or endothelial cell growth (claimed). The method may be  
CC used for inhibiting angiogenesis in a patient. The angiogenesis is  
CC associated with a disease other than a tumor that is associated with  
CC neovascularization (e.g. diabetic neuropathy, retrolental fibroplasia,  
CC trachoma, neovascular glaucoma, psoriasis, angiofibromas, immune  
CC inflammation, atherosclerosis, excessive wound repair, retinal  
CC neovascularization, macular degeneration, corneal graft rejection,  
CC contact lens overwear, Crohn's disease, non-immune inflammation,  
CC rheumatoid arthritis, systemic lupus erythromatosus, thyroiditis,  
CC Goodpasture's syndrome, systemic vasculitis, scleroderma, Sjorgen's  
CC syndrome, sarcoidosis and primary biliary cirrhosis). The method may  
CC also be used for treating/inhibiting tumor growth especially  
CC Kaposi's sarcoma (claimed).

XX Sequence 417 AA;  
SQ  
Query Match 100.0%; Score 971; DB 21; Length 417;  
Best Local Similarity 100.0%; Pred. No. 9.9e-99;  
Matches 180; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 EPAVYFKEQFLDGDGWTSRWIESKHKSDFGKFLVSSGKFGYGDDEKDKGLQTSQDARFYAL 60  
Db 18 epavyfkeqfldgdgwtswieskhksdfgkflvssgkfygdeekdkglqtsqdarfyal 77  
Qy 61 SASFPFSSKNGQTLVVQFTVKHEQNTDCGGVYVKLFPSNLDQTMHGDSEYNMFPGDIC 120  
Db 78 sasfepfsnkgqtlvvqftvkheqnldcgggyvki f pnsldqtdm hgdseynm fgpdc 137  
Qy 121 GPGTKKVHVFYFNKGNVLINKDIRCKDDEFTHLYTLIVRPONTYEVKIDNSQVESGSLE 180  
Db 138 gpgtkkvhvfnykgnvlinkdirckddefthlytlivrpontyevkidnsqvesgsle 197

RESULT 5  
AAV00927  
ID AAV00927 standard; Protein; 417 AA.  
XX  
AC AAV00927;  
XX  
DT 28-MAY-1999 (first entry)  
XX  
DE Calreticulin.

KW Clq and collectin receptor; cClqR binding domain; complement ubiquitin;  
KW CUB functionality; inhibitor; complement activation; inflammation;  
KW myocardial infarction; brain ischaemia; gut ischaemia; amyloid plaque;  
KW rheumatoid arthritis; systemic lupus erythematosis; Alzheimer's disease;  
KW immune complex nephritis; therapy.

XX Homo sapiens.  
OS  
XX  
XX WO9907406-A1.  
XX  
XX 18-FEB-1999.  
PD  
XX  
XX 12-AUG-1998; 98WO-GB02430.  
PF  
XX  
XX 12-AUG-1997; 97GB-0016998.  
PR  
XX  
XX (UYLE-) UNIV LEICESTER.  
PA  
XX  
XX Schwaeble W;  
PI  
XX  
XX WPI; 1999-180404/15.  
DR  
XX  
XX Use of a cClqR binding domain - to modulate complement ubiquitin  
PT (CUB) functionality.  
PT  
XX

PS Disclosure; Page 26-27; 3lpp; English.

XX This sequence is calreticulin, a homologue of Clq and collectin receptor (cClqR). The invention relates to the use of a cClqR binding domain in a medicament to effect complement ubiquitin (CUB) functionality, and an inhibitor of the cClqR binding domain in a medicament to inhibit CUB functionality. The cClqR binding domain, or its inhibitor, can be used to treat a human or animal body. Particularly an inhibitor is used to treat complement activation involved in the initiation and maintenance of inflammation, for example in myocardial infarction, brain ischaemia (stroke), gut ischaemia, rheumatoid arthritis, systemic lupus erythematosus, burns, immune complex nephritis, and to treat amyloid plaques in Alzheimer's disease. The use of cClqR binding domain or inhibitor enables the CUB domain functionality to be modulated using a low molecular weight molecule.

XX Sequence 417 AA;

Query Match 99.5%; Score 966; DB 20; Length 417;

Best Local Similarity 99.4%; Pred. No. 3.5e-98;

Matches 179; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 EPAVYFKEQFLDGDGWTSRWIESKHKSDFGVLSGKFGYGDDEKDKGLQTSQDARFYAL 60  
 |||||  
 DB 18 epavyfkeqfldgdgwtprwieskhksdfgkfvlsagkygdeekdkglqtsqdarfyal 77  
 |||||  
 QY 61 SASPEFSSNKGQTLVVQFTVKHEQNIDCGGYVVKLFPPNSLDQTMHGDSEYNIMFGPDIC 120  
 |||||  
 DB 78 saspefsnkqtlvvqftvkheqnidcgggyvkvkfpnsldqtdmhgdseynimfgpdic 137  
 |||||  
 QY 121 GPGTKKHVHVFNYKGNVLIINKDIRCKDDEFTHLYTLIVRPDNTYEVKIDNSQVESGSLE 180  
 |||||  
 DB 138 gpgtkkhvfhvnykgnvliinkdirckddefthlytlivrpdntyevkldnsqvesgsle 197  
 |||||

RESULT 6

AAW11156

ID AAW11156 standard; peptide; 401 AA.

XX AAW11156;

DT 31-MAY-1997 (first entry)

DE Calreticulin.

XX Calreticulin; C-domain; restenosis; inhibitor.

XX Homo sapiens.

XX W09646643-Al.

XX 21-NOV-1996.

XX 17-MAY-1996; 96WO-IB00471.

XX 16-MAY-1996; 96US-0649417.

XX 17-MAY-1995; 95US-0442844.

XX (UYAL-) UNIV ALBERTA.

XX Lucas A, Michalak M;

XX WPI; 1997-012036/01.

XX Inhibition of restenosis in patients - using calreticulin or a C-domain polypeptide of calreticulin or a variant with the same activity.

XX Disclosure; Fig 1; 48pp; English.

XX The present sequence is calreticulin. It and a C-domain derived peptide (AAW06736) are useful for treating a patient to inhibit restenosis. The

CC calreticulin-type cpds. are administered either parenterally, intravenously or via a catheter and can target areas of vascular damage to inhibit or prevent restenosis.

SQ Sequence 401 AA;

Query Match 94.9%; Score 921; DB 18; Length 401;

Best Local Similarity 95.0%; Pred. No. 3.1e-93;

Matches 171; Conservative 1; Mismatches 8; Indels 0; Gaps 0;

QY 1 EPAVYFKEQFLDGDGWTSRWIESKHKSDFGVLSGKFGYGDDEKDKGLQTSQDARFYAL 60  
 |||||  
 DB 1 epvyfkeqfldgdgwtswieskhksdfgkfvlsagkygdeekdkglqtsqdarfyal 60  
 |||||  
 QY 61 SASPEFSSNKGQTLVVQFTVKHEQNIDCGGYVVKLFPPNSLDQTMHGDSEYNIMFGPDIC 120  
 |||||  
 DB 61 sarfepfankgplvvqftvkgeqnidcgggyvkvkifpagldqkdmhgdsynimfgpdic 120  
 |||||  
 QY 121 GPGTKKHVHVFNYKGNVLIINKDIRCKDDEFTHLYTLIVRPDNTYEVKIDNSQVESGSLE 180  
 |||||  
 DB 121 gpgtkkhvfhvnykgnvliinkdirckddefthlytlivrpdntyevkldnsqvesgsle 180  
 |||||

RESULT 7

AAW04171

ID AAW04171 standard; Protein; 403 AA.

XX AAW04171;

DT 12-DEC-1996 (first entry)

DE Flea calreticulin PctCal403.

XX Calreticulin; flea; haematophagous insect; allergic dermatitis;

XX KW vaccine; therapy; PctCal403.

XX OS Ctenocephalides felis.

XX XX W09628469-Al.

XX 19-SEP-1996.

XX 08-MAR-1996; 96WO-US03133.

XX 09-MAR-1995; 95US-0401509.

XX (HESK-) HESKA CORP.

XX Rushlow KE, Stiegler GL;

XX WPI; 1996-442861/44.

XX N-PSDB; AAT39516;

XX N-PSDB; AAT39517.

XX Haematophagous insect calreticulin protein - used to reduce insect infestation and desensitise patients to allergic dermatitis

XX Claim 5; Page 68-69; 86pp; English.

XX Flea calreticulin protein PctCall589 (AAW04171) is a calcium-binding protein found in the salivary glands of Ctenocephalides felis.

XX Its amino acid sequence was deduced from a cDNA clone (AAT39516) obt'd. from a salivary gland cDNA library. Recombinant PctCall589

XX can be produced in host cells transformed with a vector carrying calreticulin nucleic acids. Calreticulin alters the blood feeding

XX behaviour of haematophagous insects and can be administered to an animal to reduce infestation. It reduces calreticulin activity in

XX insects, so reducing the insect burden on an animal. Calreticulin can be used to elicit an immune response, thereby desensitising an

XX animal to allergic dermatitis caused by fleas, mosquitoes or

XX Culicoides.



PT DNA encoding Onchocerca volvulus antigen - used to express  
PT recombinant antigen for vaccine against onchocerciasis or river  
PT blindness.

PS Disclosure; Fig 7; 20pp; English.

XX The sequence was deduced from a cDNA clone lambda RAL-1 prep.  
CC from RNA isolated from nodules excised from patients infected  
CC with O. volvulus. The N-terminal is incomplete, however Abs  
CC which specifically bind to protein prep. from induced cultures  
CC of lambda RAL-1 lysogens recognise a single polypeptide of mol.  
CC wt. 42,000 in extracts of adult worms. Analysis deduced sequence  
CC suggests that it encodes a protein of mol. wt. 39,130. If the  
CC antigen is not subject to post-translational processing this  
CC suggests that most of the coding sequence is present. The three  
CC repeats are highly hydrophilic regions likely to be exposed on  
CC the surface of the antigen and highly immunogenic. Recombinant  
CC antigen expressed by the clone can be used stimulate T-cells of  
CC individuals infected by the parasite to proliferate and may be  
CC used as the basis for a vaccine against Onchocerciasis or river  
CC blindness.

XX Sequence 336 AA;

Query Match 55.8%; Score 541.5; DB 12; Length 336;  
Best Local Similarity 68.5%; Pred. No. 1.9e-51;  
Matches 98; Conservative 21; Mismatches 23; Indels 1; Gaps 1;

QY 39 FYGDEEKGLQTSQDARFVALSASPE-PFSNKGOTLVVQFTVKHQNDICGGYVKLFP 97  
DB 1 FYGDVKKKqkkttdaktyisgaktksfnskgkslvqfsvkheqldcggqyvklna 60  
QY 98 NSLDQTMHGDSEYNIIMFGDTCGPGCTKKVHFNYKGNVLINKDIRCKDDEFTHLYTL 157  
DB 61 sdvnledshqetpyhimfipdqicgptkvvhvfhykdrnmikdkirckddvftlhlytl 120  
QY 158 IVRPNTYEVKIDNSQVESGLE 180  
DB 121 ivnsdntcyevqidqkaesgele 143

RESULT 10

AAB66341

ID AAB66341 standard; Protein; 415 AA.

XX AC AAB66341;

XX 05-APR-2001 (first entry)

XX Castor bean calreticulin SEQ ID NO: 2.

XX Castor bean; calreticulin; calcium binding; er; endoplasmic reticulum;  
KW calnexin; promoter; resistance.  
XX Ricinus communis.

XX US6171864-B1.

XX 09-JAN-2001.

XX 05-JUL-1996; 96US-0675816.

XX 05-JUL-1996; 96US-0675816.

XX (PION-) PIONEER HI-BRED INT INC.

XX Coughlan SJ, Winfrey RJ;

XX WPI; 2001-122335/13.

XX N-PSDB; AAF29741, AAF29742.

XX New nucleic acid molecules encoding a calcium binding chaperone protein  
PT

PT in endoplasmic reticulum, calreticulin, and calreticulin promoter  
PT sequences, useful for producing foreign gene products in plant cells  
XX Claim 1; Fig 3; 45pp; English.

XX The present invention provides the protein and coding sequences for the  
CC castor bean calreticulin protein and the calreticulin promoter sequence.  
CC In addition, the castor bean calnexin protein, coding sequence and  
CC promoter are also described. Calreticulin and calnexin are calcium  
CC binding proteins found in the endoplasmic reticulum (er). The  
CC calreticulin promoter sequence can be used in vectors to promote the  
CC expression of foreign genes, particularly resistance genes, in plant  
CC cells.

XX Sequence 415 AA;

Query Match 54.3%; Score 527; DB 22; Length 415;  
Best Local Similarity 55.3%; Pred. No. 1e-49;  
Matches 99; Conservative 31; Mismatches 43; Indels 6; Gaps 3;

QY 4 VYFKEQFLDCGWTSRWIESKHKSD---FGKEVLSGKPYGDEEKDKGLQTSQDARFVAL 60  
DB 22 vifeeri--edgwenrwvksdwkddentagwnylsgkwngd-pndkgqltseedyrfyal 78  
QY 61 SASFPFSSNKGOTLVVQFTVKHQNDICGGYVKLFPNSLDQTMHGDSEYNIIMFGPDIC 120  
DB 79 saefpfnskdktlvfqsvkheqldcgggymkllssatdkgkfggdtpyimfpgdic 138  
QY 121 GPCTKKVHVFNKGNVLINKDIRCKDDEFTHLYTLIVRPDNTYEVKIDNSQVESGSL 179  
DB 139 gystkvvhailnyndtnhlikkevpcetdqlthvylvirpdatysilidnvekqlgsal 197

RESULT 11

AAB66343

ID AAB66343 standard; Protein; 415 AA.

XX AC AAB66343;

XX 05-APR-2001 (first entry)

XX Castor bean calreticulin.

XX Castor bean; calreticulin; calcium binding; er; endoplasmic reticulum;  
KW calnexin; promoter; resistance.  
XX Ricinus communis.

XX US6171864-B1.

XX 09-JAN-2001.

XX 05-JUL-1996; 96US-0675816.

XX 05-JUL-1996; 96US-0675816.

XX (PION-) PIONEER HI-BRED INT INC.

XX Coughlan SJ, Winfrey RJ;

XX WPI; 2001-122335/13.

XX N-PSDB; AAF29755.

XX New nucleic acid molecules encoding a calcium binding chaperone protein  
PT in endoplasmic reticulum, calreticulin, and calreticulin promoter  
PT sequences, useful for producing foreign gene products in plant cells  
XX Disclosure; Fig 1B; 45pp; English.

XX The present invention provides the protein and coding sequences for the  
CC castor bean calreticulin protein and the calreticulin promoter sequence.  
CC In addition, the castor bean calnexin protein, coding sequence and







PR 14-MAY-1999; 99US-0134219.  
PR 14-MAY-1999; 99US-0134221.  
PR 14-MAY-1999; 99US-0134370.  
PR 18-MAY-1999; 99US-0134768.  
PR 19-MAY-1999; 99US-0134941.  
PR 20-MAY-1999; 99US-0135124.  
PR 21-MAY-1999; 99US-0135353.  
PR 24-MAY-1999; 99US-0135623.  
PR 25-MAY-1999; 99US-0136021.  
PR 27-MAY-1999; 99US-0136392.  
PR 28-MAY-1999; 99US-0136782.  
PR 01-JUN-1999; 99US-0137222.  
PR 03-JUN-1999; 99US-0137528.  
PR 04-JUN-1999; 99US-0137502.  
PR 07-JUN-1999; 99US-0137724.  
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PR 10-JUN-1999; 99US-0138540.  
PR 10-JUN-1999; 99US-0138847.  
PR 14-JUN-1999; 99US-0139119.  
PR 16-JUN-1999; 99US-0139452.  
PR 16-JUN-1999; 99US-0139453.  
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PR 18-JUN-1999; 99US-0139454.  
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PR 18-JUN-1999; 99US-0139456.  
PR 18-JUN-1999; 99US-0139457.  
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PR 19-JUL-1999; 99US-0144331.  
PR 19-JUL-1999; 99US-0144332.  
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PR 19-JUL-1999; 99US-0144334.  
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PR 22-JUL-1999; 99US-0145085.  
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PR 22-JUL-1999; 99US-0145089.  
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PR 23-JUL-1999; 99US-0145218.  
PR 23-JUL-1999; 99US-0145224.

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PR 02-AUG-1999; 99US-0146386.  
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PR 04-AUG-1999; 99US-0147204.  
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PR 27-AUG-1999; 99US-0151066.  
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PR 30-AUG-1999; 99US-0151303.  
PR 31-AUG-1999; 99US-0151438.  
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PR 07-SEP-1999; 99US-0152363.  
PR 10-SEP-1999; 99US-0153070.  
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PR 23-SEP-1999; 99US-0155486.  
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PR 28-SEP-1999; 99US-0156458.  
PR 29-SEP-1999; 99US-0156596.  
PR 04-OCT-1999; 99US-0157117.  
PR 05-OCT-1999; 99US-0157753.  
PR 06-OCT-1999; 99US-0157865.  
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PR 08-OCT-1999; 99US-0158232.  
PR 12-OCT-1999; 99US-0158369.  
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PR 14-OCT-1999; 99US-0159637.  
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PR 21-OCT-1999; 99US-0160741.  
PR 21-OCT-1999; 99US-0160767.  
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PR 28-OCT-1999; 99US-0161920.
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PR 28-OCT-1999; 99US-0161922.
PR 28-OCT-1999; 99US-0161923.
PR 29-OCT-1999; 99US-0161924.
PR 29-OCT-1999; 99US-0161925.

Query Match 52.5%; Score 510; DB 21; Length 421;
Host Local Similarity 53.9%; Pred. No. 7.8e-48;
Matches 97; Conservative 30; Mismatches 47; Indels 6; Gaps 3;

QY 3 AYVFKQFLDGGWTSRWIESKHKSD---FGKFLVLSGGFYGDDEKDKGLQTSQDARFYA 59
Db |||:|:| |||:|:|:|:| |||:|:|:|:| |||:|:|:|:| |||:|:|:|:| |||:|:|:|:|
20 vjifearf--ddgwnrvwkwsekkddntagewkhtagnwsgd-andkqigtseyrfya 76
QY 60 LSASFEPFSSKNGQTLVQFTVAKHEQKIDCGGGVYKLFPSLSLQDTDMHGDSSEYNMEGPDY 119
Db |||:|:| |||:|:| |||:|:| |||:|:| |||:|:| |||:|:| |||:|:| |||:|:| |||:|:|
77 isaepefankkktlvfqsvehqkldcgggymkllsgdvdkkfggdtppysimfgpdi 136
QY 120 GHPGTKKVHVIRNYGKNVLIINKDKDETHLYTLVLRPDNTVEVKIDNSQVESGSL 179
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
137 cqvstkkvhailltneanhlkkdvpcetdqthvyfllrpdatsyllidhvektqgsi 196

RESULT 14
AAG24607
ID AAG24607 standard; Protein; 424 AA.
XX
AC AAG24607;
XX
DT 17-OCT-2000 (first entry)
XX
DE Arabidopsis thaliana protein fragment SEQ ID NO: 28349.
XX
KW Protein identification; signal transduction pathway; metabolic pathway;
KW hybridization assay; genetic mapping; gene expression control; promoter;
KW termination sequence.
XX
OS Arabidopsis thaliana.
PN EP1033405-A2.
XX
PD 06-SEP-2000.
XX
PF 25-FEB-2000; 2000EP-0301439.
XX
PR 25-FEB-1999; 99US-0121825.
PR 05-MAR-1999; 99US-012180.
PR 09-MAR-1999; 99US-0123548.
PR 23-MAR-1999; 99US-0125788.
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PR 28-JUN-1999; 99US-0140823.
PR 29-JUN-1999; 99US-0140991.
PR 30-JUN-1999; 99US-0141287.
PR 01-JUL-1999; 99US-0141842.
PR 01-JUL-1999; 99US-0142154.
PR 02-JUL-1999; 99US-0142055.
PR 06-JUL-1999; 99US-0142390.
PR 08-JUL-1999; 99US-0142803.
PR 09-JUL-1999; 99US-0142920.
PR 12-JUL-1999; 99US-0142977.
PR 13-JUL-1999; 99US-0143542.
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PR 16-JUL-1999; 99US-0144085.
PR 16-JUL-1999; 99US-0144086.
PR 19-JUL-1999; 99US-0144325.
PR 19-JUL-1999; 99US-0144331.
PR 19-JUL-1999; 99US-0144332.
PR 19-JUL-1999; 99US-0144333.
PR 19-JUL-1999; 99US-0144334.
PR 19-JUL-1999; 99US-0144335.
PR 20-JUL-1999; 99US-0144352.
PR 20-JUL-1999; 99US-0144632.
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Query Match 52.5%; Score 510; DB 21; Length 424;

Best Local Similarity 53.9%; Pred. No. 7.8e-48;

Matches 97; Conservative 30; Mismatches 47; Indels 6; Gaps 3;

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QY 120 CGPGTKKHVIFNYKGNVLINKDIRCKDDEFTHLYTLVRPDNTYEVKIDNSQVSSGSL 179

Db 140 cgystkvhailtyneanhlkkdpcetdqtthvytilrpdatsilidnvektqtsl 199

#### RESULT 15

AAG47931

ID AAG47931 standard; Protein; 424 AA.

XX AAG47931;

XX AC

XX DT 18-OCT-2000 (first entry)

XX DE Arabidopsis thaliana protein fragment SEQ ID NO: 60468.

XX KW Protein identification; signal transduction pathway; metabolic pathway;

XX KW hybridisation assay; genetic mapping; gene expression control; promoter;

XX KW termination sequence.

XX OS Arabidopsis thaliana.

XX PN EP1033405-A2.

XX PD 06-SEP-2000.

XX PF 25-FEB-2000; 2000EP-0301439.

XX PR 25-FEB-1999; 99US-0121825.

PR 05-MAR-1999; 99US-0123180.

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PR 23-MAR-1999; 99US-0125788.

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Result No.	Score	Query %		Length	DB	ID	Description
		Match					
1	835	86.0	411	13	Q91710		Q91710 xenopus lae
2	804	82.8	405	5	Q26268		Q26268 aplysia cal
3	797	82.1	343	13	Q91711		Q91711 xenopus lae
4	796	82.0	419	13	Q98984		Q98984 rana rugosa
5	785	80.8	417	13	Q9PUC1		Q9PUC1 brachydanio
6	759	78.2	410	5	Q16893		Q16893 amblyomma a
7	731	75.3	421	5	Q9U6S0		Q9U6S0 strongyloce
8	699	72.0	406	5	Q9U916		Q9U916 drosophila
9	681.5	70.2	403	5	Q76961		Q76961 necator ame
10	680	70.0	387	5	Q97372		Q97372 dirofilaria
11	673	69.3	375	5	Q18478		Q18478 litomosoid
12	641	66.0	380	11	Q9D9Q6		Q9d9q6 mus musculu
13	539	55.5	412	10	Q40040		Q40040 hordeum vul
14	539	55.5	415	10	Q40041		Q40041 hordeum vul
15	536	55.2	421	10	Q43712		Q43712 zea mays (m
16	517	53.2	389	10	Q40567		Q40567 nicotiana t
17	514.5	53.0	427	10	Q9FYX2		Q9fyv2 pinus taeda
18	507.5	52.3	396	5	Q45034		Q45034 schistosoma
19	477.5	49.2	350	5	Q26514		Q26514 schistosoma

QY 1 EPAYVPEKQFLDGDGWTSRWIESKHKSDFGKFLVSSGKFGYDDEKDKGLQTSQDARFYAL 60  
 DB 13 EPAYVPEKQFLDGDGWTORWVESKHKHTDYGKFLKSAGKFGYDSEKDKGLQTSQDARFYAM 72  
 QY 61 SASFEPFSNKGQTLVQVFTVKHKQNDICGGYVKKLPNSLDQTDHMGDSEYINMFGPDIC 120  
 DB 73 SSRFDSFNKQDQTLVQVFSVKHKQNDICGGYVKKLPNSLDQTDHMGDSEYINMFGPDIC 132  
 QY 121 GPOTKKVHVIFNYKGNVLINKIRCKDDSFTHLYTLIVRPDNTYEVKIDNSQVESGSLE 180  
 DB 133 GPPTKKVHVIFNYKGNVLINKIRCKDDSFTHLYTLIVRPDNTYEVKIDNSQVESGSLE 192

## RESULT 2

Q26268 ID Q26268 PRELIMINARY; PRT; 405 AA.  
 AC Q26268;  
 DT 01-NOV-1996 (TReMBLrel. 01, Created)  
 DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)  
 DT 01-JUN-2001 (TReMBLrel. 17, Last annotation update)  
 DE CALRETICULIN.  
 OS Aplysia californica (California sea hare).  
 OC Eukaryota; Metazoa; Mollusca; Gastropoda; Opisthobranchia; Anaspidea;  
 OC Aplysiidae; Aplysia.  
 OX NCBI\_TaxID:6500;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE-93098937; PubMed 1463604;  
 RA Kennedy T.E., Kuhl D., Barzilai A., Sweat J.D., Kandel E.R.;  
 RT "Long-term sensitization training in Aplysia leads to an increase in  
 calreticulin, a major presynaptic calcium-binding protein.";  
 RL Nouron 9:1013-1024(1992).  
 DR EMBL: S51239; AAB24569.1; -;  
 DR InterPro: IPR000886; ER\_target.  
 DR InterPro: IPR001580; Calreticulin.  
 DR Pfam: PF00262; calreticulin; 1.  
 DR PRINTS: PR00626; CALRETICULIN.  
 DR ProDom: PD001866; Calreticulin; 1.  
 DR PROSITE: PS00803; CALRETICULIN\_1; 1.  
 DR PROSITE: PS00804; CALRETICULIN\_2; 1.  
 DR PROSITE: PS00805; CALRETICULIN\_REPEAT; 3.  
 DR PROSITE: PS00014; ER\_TARGET; UNKNOWN.1.  
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Query Match 82.8%; Score 804; DB 5; Length 405;  
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 Matches 143; Conservative 18; Mismatches 17; Indels 2; Gaps 1;

QY 1 EPAYVPEKQFLDGDGWTSRWIESKHKSDFGKFLVSSGKFGYDDEKDKGLQTSQDARFYAL 60  
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 QY 61 SASFEPFSNKGQTLVQVFTVKHKQNDICGGYVKKLPNSLDQTDHMGDSEYINMFGPDIC 120  
 DB 74 SAKFDKFSNEGKTLVQVFTVKHKQNDICGGYVKKLPNSLDQTDHMGDSEYINMFGPDIC 133  
 QY 121 GPOTKKVHVIFNYKGNVLINKIRCKDDSFTHLYTLIVRPDNTYEVKIDNSQVESGSLE 180  
 DB 134 GPPTKKVHVIFNYKGNVLINKIRCKDDSFTHLYTLIVRPDNTYEVKIDNSQVESGSLE 193

## RESULT 3

Q91711 ID Q91711 PRELIMINARY; PRT; 343 AA.  
 AC Q91711;  
 DT 01-JAN-1998 (TReMBLrel. 05, Created)  
 DT 01-JAN-1998 (TReMBLrel. 05, Last sequence update)  
 DT 01-JUN-2001 (TReMBLrel. 17, Last annotation update)  
 DE CALRETICULIN (FRAGMENT).  
 OS Xenopus laevis (African clawed frog).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;

OC Xenopodinae; Xenopus.  
 OX NCBI\_TaxID=8355;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE-93074997; PubMed-1445218;  
 RA Treves S., Zorzato F., Pozzan T.;  
 RT "Identification of calreticulin isoforms in the central nervous  
 system.";  
 RL Biochem. J. 287:579-581(1992).  
 DR EMBL: X67598; CAA47867.1; -;  
 DR InterPro: IPR001580; Calreticulin.  
 DR Pfam: PF00262; calreticulin; 1.  
 DR PRINTS: PR00626; CALRETICULIN.  
 DR ProDom: PD001866; Calreticulin; 1.  
 DR PROSITE: PS00803; CALRETICULIN\_1; 1.  
 DR PROSITE: PS00804; CALRETICULIN\_2; 1.  
 DR PROSITE: PS00805; CALRETICULIN\_REPEAT; 3.  
 FT NON\_TER 1  
 FT NON\_TER 343 343  
 SQ SEQUENCE 343 AA; 40105 MW; 3E7DDAFA33B91DE1 CRC64;

Query Match 82.1%; Score 797; DB 13; Length 343;

Best Local Similarity 85.2%; Pred. No. 8.7e-68;

Matches 144; Conservative 12; Mismatches 13; Indels 0; Gaps 0;

QY 12 DGDGWTSRWIESKHKSDFGKFLVSSGKFGYDDEKDKGLQTSQDARFYALSASFESNKG 71  
 DB 1 DGDGWTORWVESKHKSDYCKFLKSAGKFGYDSEKDKGLQTSQDARFYAMSSRFSNKG 60  
 QY 72 QTLVQVFTVKHKQNDICGGYVKKLPNSLDQTDHMGDSEYINMFGPDICGPTKKVHVIF 131  
 DB 61 QTLVQVFTVKHKQNDICGGYVKKLPNSLDQTDHMGDSEYINMFGPDICGPTKKVHVIF 120  
 QY 132 NYGKNVLINKIRCKDDSFTHLYTLIVRPDNTYEVKIDNSQVESGSLE 180  
 DB 121 QYKKKMLQINKIRCKDDSFTHLYTLIVRPDNTYEVKIDNSQVESGSLE 169

## RESULT 4

Q98984 ID Q98984 PRELIMINARY; PRT; 419 AA.  
 AC Q98984;  
 DT 01-FEB-1997 (TReMBLrel. 02, Created)  
 DT 01-FEB-1997 (TReMBLrel. 02, Last sequence update)  
 DT 01-JUN-2001 (TReMBLrel. 17, Last annotation update)  
 DE CALRETICULIN.  
 OS Rana rugosa (Frog).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Rana.  
 OX NCBI\_TaxID=8410;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE-96234004; PubMed=8654561;  
 RA Yamamoto S., Nakamura M.;  
 RT "Calnexin: its molecular cloning and expression in the liver of the  
 frog, Rana rugosa.";  
 RL FEBS Lett. 387:27-32(1996).  
 DR [2]  
 RP SEQUENCE FROM N.A.  
 RA Yamamoto S.;  
 RT "Strong expression of the calreticulin gene in the liver of Rana  
 rugosa tadpoles.";  
 RL J. Exp. Zool. 0:0-0(1996).  
 DR EMBL: D78589; BAA11425.1; -;  
 DR InterPro: IPR000886; ER\_target.  
 DR InterPro: IPR001580; Calreticulin.  
 DR Pfam: PF00262; calreticulin; 1.  
 DR PRINTS: PR00626; CALRETICULIN.  
 DR ProDom: PD001866; Calreticulin; 1.  
 DR PROSITE: PS00803; CALRETICULIN\_1; 1.  
 DR PROSITE: PS00804; CALRETICULIN\_2; 1.

[illegible]

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RP SEQUENCE FROM N.A.
RA Susan J.M., Just M.L., Lennarz W.J.;
RT "Cloning and Characterization of AlphaP Integrin and Calreticulin in
RL Embryos of the Sea Urchin";
RL Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF177915; AAD55725.1; -.
DR InterPro; IPR000886; ER.target.
DR Pfam; PF00262; calreticulin; 1.
DR PRINTS; PR00626; CALRETICULIN.
DR ProDom; PD001866; Calreticulin; 1.
DR PROSITE; PS00804; CALRETICULIN_2; 1.
DR PROSITE; PS00805; CALRETICULIN_REPEAT; 3.
DR PROSITE; PS00014; ER_TARGET; UNKNOWN_1.
KW Signal.
FT SIGNAL.
FT CHAIN.
FT SIGNAL.
FT CHAIN.
SQ SEQUENCE 421 AA; 48822 MW; 172C664F59F41F93 CRC64;

Query Match 75.3%; Score 731; DB 5; Length 421;
Best Local Similarity 74.7%; Pred. No. 2.1e-61;
Matches 133; Conservative 19; Mismatches 24; Indels 2; Gaps 2;

QY 4 VYFKEQFLDGDGWTSSWIESKHK-SDFGKFLSSGKFGYDEEKDKGLQTSQDARFYALSA 62
DB 20 VYFEDQFADA-SWESRWVESVHKGSAGKFKWSAGKFGYDAEQDKGIQTSQDAKFGYGLSA 78
QY 63 SPEPFSNKGQTLVQFTVKHEQNIDCGGKGYVKLFPPNSLQDTMHGDSSEYNIMFGPDICGP 122
DB 79 KETDFSNEGKDLVQFTVKHEQNIDCGGKGYVKLFPPADLQDQDMHGDSYINIMFGPDICGP 138
QY 123 GTKKKVHVFNYGKKNVLINKDKCKDDETHLYTLVLRPDNTYEVKIDNSQVESGSL 180
DB 139 GTKKKVHVFNYGKKNLLIKKDKCKDDETHLYTLVLRSDNSYEVKIDNEKAQAGNLE 196

RESULT 8
QY0916 PRELIMINARY; PRT; 406 AA.
AC QY0916;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
DE CALRETICULIN.
GN CRC OR CG9429.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-OREGON-R;
RA Dodo K., Sakuyama Y., Gamo S.;
RT "Drosophila melanogaster calreticulin for mRNA";
RL Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AH000718; BAA85379.1; -.
DR FlyBase; FBgn0005585; Crc.
DR InterPro; IPR001580; Calreticulin.
DR InterPro; IPR000886; ER.target.
DR Pfam; PF00262; calreticulin; 1.
DR PRINTS; PR00626; CALRETICULIN.
DR ProDom; PD001866; Calreticulin; 1.
DR PROSITE; PS00803; CALRETICULIN_1; 1.
DR PROSITE; PS00804; CALRETICULIN_2; 1.
DR PROSITE; PS00805; CALRETICULIN_REPEAT; 3.
DR PROSITE; PS00014; ER_TARGET; UNKNOWN_1.
SQ SEQUENCE 406 AA; 46809 MW; 68BA49A6B81CC427 CRC64;

Query Match 72.0%; Score 699; DB 5; Length 406;
Best Local Similarity 74.2%; Pred. No. 2.2e-58;

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Matches 132; Conservative 14; Mismatches 30; Indels 2; Gaps 2;

QY 4 VYFKEQFLDGDGWTSSWIESKHK-SDFGKFLSSGKFGYDEEKDKGLQTSQDARFYALSA 62
DB 21 VYLKENF-DNENWEDPMYISKHPGKFEFVLTPTGTFYNDADKGIQTSQDARFYAASR 79
QY 63 SPEPFSNKGQTLVQFTVKHEQNIDCGGKGYVKLFPPNSLQDTMHGDSSEYNIMFGPDICGP 122
DB 80 KEDGFSNEDKPLVQFSVAKHEQNIDCGGKGYVKLFDCSLQDTMHGDSPEYINIMFGPDICGP 139
QY 123 GTKKKVHVFNYGKKNVLINKDKCKDDETHLYTLVLRPDNTYEVKIDNSQVESGSL 180
DB 140 GTKKKVHVFNYGKKNHLISKDKCKDDVYTHFTYTLVLRPDNTYEVLDNEKVESGNLE 197

RESULT 9
QY0961 PRELIMINARY; PRT; 403 AA.
AC QY0961;
DT 01-NOV-1998 (TREMBlrel. 08, Created)
DT 01-NOV-1998 (TREMBlrel. 08, Last sequence update)
DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
DE CALRETICULIN PRECURSOR.
GN CRT.
OS Necator americanus.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Strongylida;
OC Ancylostomatidae; Ancylostomatidae; Bunostominae; Necator.
OX NCBI_TaxID=51031;
RN [1]
RP SEQUENCE FROM N.A.
RA Pritchard D.I., Brown A., McElroy P., Loukas A., Girdwood K.,
RA Berry C., Fullkrug R., Beck E.;
RT "Calreticulin is a hookworm allergen";
RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ006790; CAA07254.1; -.
DR InterPro; IPR000886; ER.target.
DR Pfam; PF00262; calreticulin; 1.
DR PRINTS; PR00626; CALRETICULIN.
DR ProDom; PD001866; Calreticulin; 1.
DR PROSITE; PS00803; CALRETICULIN_1; 1.
DR PROSITE; PS00804; CALRETICULIN_2; 1.
DR PROSITE; PS00805; CALRETICULIN_REPEAT; 3.
DR PROSITE; PS00014; ER_TARGET; UNKNOWN_1.
KW Signal; Allergen.
FT SIGNAL.
FT CHAIN.
FT SIGNAL.
FT CHAIN.
SQ SEQUENCE 403 AA; 46833 MW; 21F38B0515487B6F CRC64;

Query Match 70.2%; Score 681.5; DB 5; Length 403;
Best Local Similarity 68.5%; Pred. No. 9.8e-57;
Matches 122; Conservative 30; Mismatches 23; Indels 3; Gaps 3;

QY 4 VYFKEQFLDGDGWTSSWIESKHK-SDFGKFLSSGKFGYDEEKDKGLQTSQDARFYALSA 63
DB 18 VYFKEEFLD-DSWKEKRWOSKHSKSDYGEFVLGAGKFGDATRDQGMKTSQDAKFSRAAK 76
QY 64 F-EPPFSNKGQTLVQFTVKHEQNIDCGGKGYVKLFPPNSLQDTMHGDSSEYNIMFGPDICGP 122
DB 77 FPKAFSNKGTVVQFTVKHEQIDCGGKGYVKVMSDDVLSDFHGETPYNVNFGPDICGP 136
QY 123 GTKKKVHVFNYGKKNVLINKDKCKDDETHLYTLVLRPDNTYEVKIDNSQVESGSL 180
DB 137 -TKKVHDFSYGKKNHLIKKDKCKDDELTHLYTLVLRPDNTYEVQIDGKVESGSL 193

RESULT 10
QY09732 PRELIMINARY; PRT; 387 AA.
AC QY09732;
DT 01-MAY-1999 (TREMBlrel. 10, Created)
DT 01-MAY-1999 (TREMBlrel. 10, Last sequence update)
DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)

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DE CALRETICULIN PRECURSOR.
OS Dirofilaria immitis.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Spirurida; Filarioidea;
OC Onchocercidae; Dirofilaria.
OX NCBI_TaxID=6287;
RN [1]
RP
RX MEDLINE=99094497; PubMed=9879888;
RA Tsuji N., Morales T.H., Ozols V.V., Carmody A.B., Chandrashekar R.;
RT "Molecular characterization of a calcium-binding protein from the
RT filarial parasite Dirofilaria immitis.";
RL Mol. Biochem. Parasitol. 97:69-79(1998).
DR EMBL: AF052978; AD03405.1; -.
DR InterPro: IPR001580; Calreticulin.
DR Pfam: PF00262; calreticulin; 1.
DR PRINTS: P00626; CALRETICULIN.
DR ProDom: PD001866; Calreticulin; 1.
DR PROSITE: PS00803; CALRETICULIN_1; 1.
DR PROSITE: PS00804; CALRETICULIN_2; 1.
DR PROSITE: PS00805; CALRETICULIN_REPEAT; 3.
KW SIGNAL.
FT CHAIN 1 18 POTENTIAL.
FT CHAIN 19 387 CALRETICULIN.
FT SEQUENCE 387 AA; 44941 MW; E77418F6AFA5885 CRC64;

Query Match 70.0%; Score 680; DB 5; Length 387;
Best Local Similarity 68.5%; Pred. No. 1.3e-56;
Matches 122; Conservative 27; Mismatches 27; Indels 2; Gaps 2;

QY 4 VYFKEQFLDGDGWTSRWIESKHSKDFGKFLVSSGKFGYDDEKDKGLQTSQDARFYALSAS 63
DB 19 IYFKEEFDSD-DWEKRWIKSKHDKDFGKWEISHGKFGYDAVKDKGLTKTQDAKFYSIGAK 77
QY 64 FEP-FSNKGTQLVQFTVVKHEQNIIDCGGKFLVSPNSLDQTDHMGDSEYNIMFGPDICGP 122
DB 78 FKGFSGNKGSLVQFSVHKEQIDCGGKFLVSPNSLDQTDHMGDSEYNIMFGPDICGP 137
QY 123 GTRKGVHVIYFKGNKLVINKDKDETHLYTLVLRPNTVEYKIDNSQVSGSLE 180
DB 138 GTRKGVHVIYFKGNHMKIKDKDDVTHLYTLVNSDNPYEYQIDGKAESGELE 195

RESULT 11
O18478 PRELIMINARY; PRT; 375 AA.
AC O18478;
DT 01-JAN-1998 (TREMBLrel. 05, Created)
DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE RAL-1 PROTEIN (FRAGMENT).
OS Litomosoides sigmodontis.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Spirurida; Filarioidea;
OC Onchocercidae; Litomosoides.
OX NCBI_TaxID=42156;
RN [1]
RP
RX MEDLINE=99094497; PubMed=9879888;
RA MacLennan K., Hoffman W.H., Taylor D.W.;
RT Submitted (SEP-1997) to the EMBL/Genbank/DBJ databases.
DR EMBL: AJ001621; CAA04877.1; -.
DR InterPro: IPR001580; Calreticulin.
DR Pfam: PF00262; calreticulin; 1.
DR PRINTS: P00626; CALRETICULIN.
DR ProDom: PD001866; Calreticulin; 1.
DR PROSITE: PS00803; CALRETICULIN_1; 1.
DR PROSITE: PS00804; CALRETICULIN_2; 1.
DR PROSITE: PS00805; CALRETICULIN_REPEAT; 3.
FT NON_TER 375
FT SEQUENCE 375 AA; 43842 MW; 03F7642FBFF7A5B8 CRC64;

Query Match 69.3%; Score 673; DB 5; Length 375;
Best Local Similarity 68.5%; Pred. No. 5.8e-56;
Matches 122; Conservative 27; Mismatches 27; Indels 2; Gaps 2;
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Matches 122; Conservative 26; Mismatches 28; Indels 2; Gaps 2;

QY 4 VYFKEQFLDGDGWTSRWIESKHSKDFGKFLVSSGKFGYDDEKDKGLQTSQDARFYALSAS 63
DB 19 IYFKEEFDSD-DWEKRWIKSKHDKDFGKWEISHGKFGYDAVKDKGLTKTQDAKFYSIGAK 77
QY 64 FEP-FSNKGTQLVQFTVVKHEQNIIDCGGKFLVSPNSLDQTDHMGDSEYNIMFGPDICGP 122
DB 78 FKGFSGNKGSLVQFSVHKEQIDCGGKFLVSPNSLDQTDHMGDSEYNIMFGPDICGP 137
QY 123 GTRKGVHVIYFKGNKLVINKDKDETHLYTLVLRPNTVEYKIDNSQVSGSLE 180
DB 138 GTRKGVHVIYFKGNHMKIKDKDDVTHLYTLVNSDNPYEYQIDGKAESGELE 195

RESULT 12
O9D906 PRELIMINARY; PRT; 380 AA.
AC O9D906;
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE 1700031L01RIK PROTEIN.
GN 1700031L01RIK.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schrim L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fietcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohsaki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
DR EMBL: AK006582; BAB24660.1; -.
DR MGD; MGI:1320566; 1700031L01RIK.
DR InterPro: IPR001580; Calreticulin.
DR Pfam: PF00262; calreticulin; 2.
DR PRINTS: P00626; CALRETICULIN.
DR ProDom: PD001866; Calreticulin; 1.
DR PROSITE: PS00803; CALRETICULIN_1; 1.
DR PROSITE: PS00804; CALRETICULIN_2; 1.
DR PROSITE: PS00805; CALRETICULIN_REPEAT; 3.
FT SEQUENCE 380 AA; 44198 MW; B13BC4ADB1B0442 CRC64;

Query Match 66.0%; Score 641; DB 11; Length 380;
Best Local Similarity 65.0%; Pred. No. 6.4e-53;
Matches 115; Conservative 30; Mismatches 32; Indels 0; Gaps 0;

QY 4 VYFKEQFLDGDGWTSRWIESKHSKDFGKFLVSSGKFGYDDEKDKGLQTSQDARFYALSAS 63
DB 21 VYFEEFLDGERWRNRWVQSTNDSQGFHFRVSSGKFGYDDEKDKGLQTSQDARFYALSAS 80
QY 64 FEP-FSNKGTQLVQFTVVKHEQNIIDCGGKFLVSPNSLDQTDHMGDSEYNIMFGPDICGP 123
DB 81 FKFPNKGKTLVIQYTVKHEQNIIDCGGKFLVSPNSLDQTDHMGDSEYNIMFGPDICGP 140
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QY 124 TKKVHVFYFNKGNVLINKDKDEFTHLYTLVLRPONTYEVKIDNSQVSGSL 180
      ||||| : : | |||| | ||||| : ||||| : ||||| : ||||| :
DB 141 IKKVHVLFFKNQYHENKKPIRCKVGFTHLYTLVLRPDLSEYKVDQSGSIE 197

RESULT 13
Q40040
ID Q40040 PRELIMINARY; PRT; 412 AA.
AC Q40040;
DT 01-NOV-1996 (TRENBLrel. 01, Created)
DT 01-NOV-1996 (TRENBLrel. 01, Last sequence update)
DT 01-JUN-2001 (TRENBLrel. 17, Last annotation update)
DE CALRETICULIN (FRAGMENT).
GN CRH1
OS Hordeum vulgare (Barley).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;
OC Triticeae; Hordeum.
OX NCBI_TaxID 4513;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-MOREX; TISSUE-OVARY;
RX MEDLINE-94339696; PubMed-7914763;
RA Chen F., Hayes P.M., Mulroony D., Pan A.;
RT "Identification and characterization of cDNA clones encoding plant
calreticulin in barley.";
RL Plant Cell 6:835-843(1994).
DR Mendel; 8546; Horvu; 1166; 8546.
DR InterPro; IPR000886; ER_target.
DR InterPro; IPR001580; Calreticulin.
DR Pfam; PF00262; calreticulin; 1.
DR PRINTS; P000626; CALRETICULIN.
DR PRODOM; PD001866; Calreticulin; 1.
DR PROSITE; PS00803; CALRETICULIN_1; 1.
DR PROSITE; PS00804; CALRETICULIN_2; 1.
DR PROSITE; PS00805; CALRETICULIN_REPEAT; 2.
DR PROSITE; PS00014; ER_TARGET; UNKNOWN_1.
KW Calcium-binding.
FT NON_TER 1
FT NON_TER 412
FT SEQUENCE 412 AA; 47037 MW; 376695D6AA78AB0 CRC64;

Query Match 55.5%; Score 539; DB 10; Length 412;
Best Local Similarity 56.4%; Pred. No. 3.4e-43;
Matches 101; Conservative 31; Mismatches 41; Indels 6; Gaps 3;

QY 4 VYFKEQFLDGDGWTSMWIESKHSD---FGKFLVSSGKFGYDEKDKGLQTSQDARFYAL 60
      |:||:| | ||||| : ||||| : ||||| : ||||| : ||||| :
DB 20 VFQEQKF--EDGWESRWKSEKKNMAGENNHTSGKWHGDAE-DKGIQTSEDYRFYAI 76

QY 61 SASPEFSSNKGQTLVQFTVKHQNIDCGGYVKKLPNSLDQTDHMGDSYINMFGPDIC 120
      || : |||| : ||||| : ||||| : ||||| : ||||| : ||||| :
DB 77 SAEYFESSNKKDKTLVQFTVKHQNIDCGGYVKKLLGGVDQKKFGDTPYGMFGPDIC 136

QY 121 GPGTKKVVHVFYFNKGNVLINKDKDEFTHLYTLVLRPONTYEVKIDNSQVSGSL 179
      | |||| | ||||| : ||||| : ||||| : ||||| : ||||| :
DB 137 GYSTKKVHTILTNGKNHLLKKDVPCTQLSHVYTLIRPDATYSILIDNEEKQTGSI 195

RESULT 14
Q40041
ID Q40041 PRELIMINARY; PRT; 415 AA.
AC Q40041;
DT 01-NOV-1996 (TRENBLrel. 01, Created)
DT 01-NOV-1996 (TRENBLrel. 01, Last sequence update)
DT 01-JUN-2001 (TRENBLrel. 17, Last annotation update)
DE CALRETICULIN (FRAGMENT).
GN CRH2
OS Hordeum vulgare (Barley).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

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OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;
OC Triticeae; Hordeum.
OX NCBI_TaxID 4513;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-MOREX; TISSUE-OVARY;
RX MEDLINE-94339696; PubMed-7914763;
RA Chen F., Hayes P.M., Mulroony D., Pan A.;
RT "Identification and characterization of cDNA clones encoding plant
calreticulin in barley.";
RL Plant Cell 6:835-843(1994).
DR EMBL; L27349; AAA32949.1; -.
DR Mendel; 8547; Horvu; 1166; 8547.
DR InterPro; IPR000886; ER_target.
DR InterPro; IPR001580; Calreticulin.
DR Pfam; PF00262; calreticulin; 1.
DR PRINTS; P000626; CALRETICULIN.
DR PRODOM; PD001866; Calreticulin; 1.
DR PROSITE; PS00803; CALRETICULIN_1; 1.
DR PROSITE; PS00804; CALRETICULIN_2; 1.
DR PROSITE; PS00805; CALRETICULIN_REPEAT; 2.
DR PROSITE; PS00014; ER_TARGET; UNKNOWN_1.
KW Calcium-binding.
FT NON_TER 1
FT NON_TER 415
FT SEQUENCE 415 AA; 47359 MW; 2897914812FBE33E CRC64;

Query Match 55.5%; Score 539; DB 10; Length 415;
Best Local Similarity 56.4%; Pred. No. 3.4e-43;
Matches 101; Conservative 31; Mismatches 41; Indels 6; Gaps 3;

QY 4 VYFKEQFLDGDGWTSMWIESKHSD---FGKFLVSSGKFGYDEKDKGLQTSQDARFYAL 60
      |:||:| | ||||| : ||||| : ||||| : ||||| : ||||| :
DB 23 VFQEQKF--EDGWESRWKSEKKNMAGENNHTSGKWHGDAE-DKGIQTSEDYRFYAI 79

QY 61 SASPEFSSNKGQTLVQFTVKHQNIDCGGYVKKLPNSLDQTDHMGDSYINMFGPDIC 120
      || : |||| : ||||| : ||||| : ||||| : ||||| : ||||| :
DB 80 SAEYFESSNKKDKTLVQFTVKHQNIDCGGYVKKLLGGVDQKKFGDTPYGMFGPDIC 139

QY 121 GPGTKKVVHVFYFNKGNVLINKDKDEFTHLYTLVLRPONTYEVKIDNSQVSGSL 179
      | |||| | ||||| : ||||| : ||||| : ||||| : ||||| :
DB 140 GYSTKKVHTILTNGKNHLLKKDVPCTQLSHVYTLIRPDATYSILIDNEEKQTGSI 198

RESULT 15
Q43712
ID Q43712 PRELIMINARY; PRT; 421 AA.
AC Q43712;
DT 01-NOV-1996 (TRENBLrel. 01, Created)
DT 01-NOV-1996 (TRENBLrel. 01, Last sequence update)
DT 01-JUN-2001 (TRENBLrel. 17, Last annotation update)
DE CALCIUM-BINDING PROTEIN PRECURSOR.
GN CRT1
OS Zea mays (Maize).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; PACC clade;
OC Panicoideae; Andropogoneae; Zea.
OX NCBI_TaxID 4577;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-VAR MERIT; TISSUE-ROOT TIP;
RA Napier R.M., Trueman S., Henderson J., Boyce J.M., Hawes C.R.,
RA Fricker M.D., Venis M.A.;
RL J. Exp. Bot. 46:1603-1613(1995).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE-96309381; PubMed-8704156;
RA Dresselhaus T., Hagel C., Loerz H., Kranz E.;
RT "Isolation of a full-length cDNA encoding calreticulin from a PCR
library of in vitro zygotes of maize.";
RL Plant Mol. Biol. 31:23-34(1996).
DR EMBL; 246772; CAA86728.1; -.

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DR EMBL; X89813; CAA61939.1; -
DR Mendel; 11228; Zeama; 1166; 11228.
DR InterPro; IPR000886; ER_target.
DR InterPro; IPR01580; Calreticulin.
DR Pfam; PF00262; calreticulin; 1.
DR PRINTS; PR00626; CALRETICULIN.
DR PRODom; PD001866; Calreticulin; 1.
DR PROSITE; PS00803; CALRETICULIN_1; 1.
DR PROSITE; PS00804; CALRETICULIN_2; 1.
DR PROSITE; PS00805; CALRETICULIN_REPEAT; 2.
DR PROSITE; PS00014; ER_TARGET; UNKNOWN_1.
KW Signal; Calcium-binding.
FT SIGNAL 1 25 POTENTIAL.
FT CHAIN 26 421 CALRETICULIN.
SQ SEQUENCE 421 AA; 48012 MW; 5AAE02B77ED3126D CRC64;

Query Match 55.2%; Score 536; DB 10; Length 421;
Best Local Similarity 56.4%; Pred. No. 6.7e-43;
Matches 101; Conservative 31; Mismatches 41; Indels 6; Gaps 3;

Qy 4 VVFKRQFLDGDGWTSRWIESKHKSD---FGKFLSSGRFYGDDEKDKGLQTSODARFYAL 60
Db 27 VFFQEKF--EDGWESRWYKSEWKKNMAGENWHTSGKNGDAE-DKGIQTSEDYRFYAI 83

Qy 61 SASPEPFSNKGOTLVVQFTVKHEQNIDCGGYVKLFNPNSLDQTMHGDSEYNIMFGPDIC 120
Db 84 SAEYPEFSNKDKTLVLQFSVRKHEQKLDCCGGYVKLLGGDVQDKKFGGDTSYSIMFGPDIC 143

Qy 121 GPGTKKVVHVIENYKGNVLIINKDIRCKDDETHLYTLIVRPDNTYEVKIDNSQVESGSL 179
Db 144 GYSTKKVHTILTQDGNHILIKKDVPECETDQLTHVYTLIIRPDATYSILIDNEEKQTGSI 202
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Search completed: January 9, 2002, 15:03:27  
Job time: 269 sec





GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: January 9, 2002, 15:02:02 ; Search time 43.73 Seconds  
(without alignments)  
106.258 Million cell updates/sec

Title: US-09-828-000-4  
Perfect score: 340  
Sequence: 1 TDMHGSEYNIMFGPDICGP.....IRCKDDEFTHTLYIVRPN 61  
Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues  
Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR68:\*  
1: pir1:\*  
2: pir2:\*  
3: pir3:\*  
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	340	100.0	417	1 A37047	calreticulin precu
2	335	98.5	400	2 S43376	calreticulin, brai
3	335	98.5	416	1 S06763	calreticulin precu
4	335	98.5	416	2 JH0819	calreticulin precu
5	335	98.5	418	1 A34154	calreticulin precu
6	335	98.5	421	2 S36799	calreticulin precu
7	305	89.7	405	1 JH0795	calreticulin precu
8	296	87.1	384	2 S29130	calreticulin (clon
9	293	86.2	406	2 A56637	calreticulin homol
10	288	84.7	411	2 S29129	calreticulin precu
11	287	84.4	419	2 S71343	calreticulin precu
12	261	76.8	336	2 A32507	41K larval antigen
13	242	71.2	393	1 A48573	calreticulin autoa
14	233.5	68.7	395	2 S25851	calreticulin precu
15	207	60.9	416	2 T14554	calreticulin - bee
16	205	60.3	421	2 S58170	calreticulin precu
17	202	59.4	415	2 T10172	calreticulin - cas
18	200	58.8	412	2 T05703	calreticulin - bar
19	200	58.8	415	2 T05705	calreticulin - bar
20	199	58.5	425	2 C96605	calreticulin (Crt1
21	195	57.4	422	2 T07841	probable calreticu
22	194	57.1	444	2 H86224	hypothetical prote
23	191	56.2	416	2 T16968	calreticulin call
24	190	55.9	389	2 T03691	calreticulin - com
25	123.5	36.3	592	2 I53260	calnexin - human
26	122.5	36.0	546	2 T06415	calnexin - soybean
27	121.5	35.7	592	2 A46673	calnexin precursor
28	120.5	35.4	591	2 B54354	calnexin precursor
29	120.5	35.4	591	2 C54354	calnexin precursor

30	120.5	35.4	593	1 A37273	calnexin precursor
31	115.5	34.0	530	2 JN0597	calnexin-like prot
32	115.5	34.0	540	2 T10892	probable calnexin
33	115.5	34.0	582	2 A46637	calnexin homolog S
34	115.5	34.0	619	2 S40938	hypothetical prote
35	115.5	34.0	622	2 S71342	calnexin precursor
36	108.5	31.9	428	2 T03251	calnexin - maize (
37	108.5	31.9	611	2 A53418	calmeglin precursor
38	108.5	31.9	611	2 A54086	calnexin-t - mouse
39	103.5	30.4	532	2 T49873	calnexin homolog -
40	103	30.3	560	2 S56142	calcium-binding pr
41	90.5	26.6	297	2 S70552	calnexin homolog C
42	77.5	22.8	540	1 JU0470	site-specific DNA-
43	67.5	19.9	457	2 H85013	hypothetical prote
44	67.5	19.9	968	2 T01733	hypothetical prote
45	66	19.4	560	2 S50439	hypothetical prote

## ALIGNMENTS

RESULT 1  
A37047  
calreticulin precursor - human  
N:Alternate names: 52K ribonucleoprotein autoantigen Ro/SS-A; 60K integrin-binding pr  
C:Species: Homo sapiens (man)  
C>Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 18-Feb-2000  
R:McCaulliffe, D.P.; Yang, Y.S.; Wilson, J.; Sontheimer, R.D.; Capra, J.D.  
A:Accession: A42330; A37047; A46452; A28812; PH1525; A40346; S11475; T45075  
J. Biol. Chem. 267, 2557-2562, 1992  
A:Title: The 5'-flanking region of the human calreticulin gene shares homology with t  
A:Reference number: A42330; MUID:92129342  
A:Accession: A42330  
A:Molecule type: DNA  
A:Residues: 1-417 <MC2>  
A>Note: sequence extracted from NCBI backbone (NCBIN:78537, NCBIP:78536)  
R:McCaulliffe, D.P.; Lux, F.A.; Lieu, T.S.; Sanz, I.; Hanke, J.; Newkirk, M.M.; Bachin  
J. Clin. Invest. 85, 1379-1391, 1990  
A:Title: Molecular cloning, expression, and chromosome 19 localization of a human Ro/  
A:Reference number: A37047; MUID:90237213  
A:Accession: A37047  
A:Molecule type: mRNA  
A:Residues: 1-417 <MC2>  
A:Cross-references: GB:M32294; NID:g337486; PTDN:AAA36582.1; PTD:g337487  
A>Note: the authors translated the codon GTA for residue 349 as Tyr  
R:Rokeach, L.A.; Haselby, J.A.; Meilof, J.F.; Smeenk, R.J.; Unnasch, T.R.; Greene, B.  
J. Immunol. 147, 3031-3039, 1991  
A:Title: Characterization of the autoantigen calreticulin.  
A:Reference number: A46452; MUID:92013129  
A:Accession: A46452  
A:Molecule type: mRNA  
A:Residues: 1-417 <R0K>  
A:Cross-references: GB:M84739; NID:g179881; PTDN:AAA51916.1; PTD:g179882  
A>Note: sequence extracted from NCBI backbone (NCBIN:60749, NCBIP:60750)  
R:Lieu, T.S.; Newkirk, M.M.; Capra, J.D.; Sontheimer, R.D.  
J. Clin. Invest. 82, 96-101, 1988  
A:Title: Molecular characterization of human Ro/SS-A antigen. Amino terminal sequence  
A:Reference number: A28812; MUID:88273610  
A:Accession: A28812  
A:Molecule type: protein  
A:Residues: 18-41 <LIE>  
A>Note: 18-Ala was also found  
R:Dupuis, M.; Schaefer, E.; Krause, K.H.; Tschopp, J.  
J. Exp. Med. 177, 1-7, 1993  
A:Title: The calcium-binding protein calreticulin is a major constituent of lytic gra  
A:Reference number: PH1525; MUID:93115648  
A:Accession: PH1525  
A:Molecule type: protein  
A:Residues: 18-27 <DUP>  
A:Experimental source: LAK cell  
R:Kojima, M.V.; Finlay, B.B.; Gray, V.; Dedhar, S.  
Biochemistry 30, 9859-9866, 1991  
A:Title: In vitro interaction of a polypeptide homologous to human Ro/SS-A antigen (c

A:Reference number: A40346; MUID:92002034  
A:Accession: A40346  
A:Molecule type: protein  
A:Residues: 18-34, 'R' <ROU>  
R:Krause, K.H.; Simmerman, H.K.B.; Jones, L.R.; Campbell, K.P.  
Biochem. J. 270, 545-548, 1990  
A:Title: Sequence similarity of calreticulin with a Ca(2+)-binding protein that co-purifies with the endoplasmic reticulum chaperone BiP  
A:Reference number: S11475; MUID:90380058  
A:Accession: S11475  
A:Molecule type: protein  
A:Residues: 18-32 <KRA>  
R:Lamerdin, J.; McCreedy, P.; Stilwagen, S.; Ramirez, M.; Carrano, A.  
submitted to the EMBL Data Library, November 1996  
A:Description: Characterization by genomic sequence analysis of a gene-rich 111 kb region on human chromosome 12p13  
A:Reference number: Z22906  
A:Accession: T45075  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-417 <LAM>  
A:Cross-references: EMBL:AD000092; PIDN:AAB51176.1  
A:Experimental source: cell line 5HL2-B; fibroblast  
C:Comment: Autoantibodies specific for this protein are found in Sjogren's syndrome and Sjogren's syndrome-like syndrome  
C:Genetics:  
A:Gene: GDB:CALR  
A:Cross-references: GDB:125179; OMIM:109091  
A:Map position: 19p13.3-19p13.2  
A:Introns: 31/1; 65/1; 133/1; 164/3; 234/3; 272/3; 320/3; 351/3  
A:Note: CRTC  
C:Superfamily: calreticulin  
C:Keywords: calcium binding; integrin binding  
F:1-17/Domain: signal sequence #status predicted <SIG>  
F:18-417/Product: calreticulin #status predicted <MAT>  
F:414-417/Region: endoplasmic reticulum retention signal

Query Match 100.0%; Score 340; DB 1; Length 417;  
Best Local Similarity 100.0%; Pred. No. 4.5e-33;  
Matches 61; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TDMHGDSEYNIMFGPDICGPGTKKVVHIFNYKGNVLIINKDIRCKDDETHLYTLIVRPD 60  
|||||  
DB 120 TDMHGDSEYNIMFGPDICGPGTKKVVHIFNYKGNVLIINKDIRCKDDETHLYTLIVRPD 179

QY 61 N 61  
DB 180 N 180

RESULT 2  
S43376  
calreticulin, brain isoform 1 - bovine  
C:Species: Bos primigenius taurus (cattle)  
C:Date: 20-Oct-1994 #sequence\_revision 23-Mar-1995 #text\_change 07-May-1999  
A:Accession: S43376; S36801  
R:Matsuoka, K.; Seta, K.; Yamakawa, Y.; Okuyama, T.; Shinoda, T.; Isobe, T.  
Biochem. J. 298, 435-442, 1994  
A:Title: Covalent structure of bovine brain calreticulin.  
A:Reference number: S43376; MUID:94183174  
A:Accession: S43376  
A:Molecule type: protein  
A:Residues: 1-400 <MAT>  
A:Experimental source: brain  
R:Liu, N.; Fine, R.E.; Johnson, R.J.  
Biochim. Biophys. Acta 1202, 70-76, 1993  
A:Title: Comparison of cDNAs from bovine brain coding for two isoforms of calreticulin.  
A:Reference number: S36799; MUID:93385184  
A:Accession: S36801  
A:Status: nucleic acid sequence not shown  
A:Molecule type: mRNA  
A:Residues: 45-63, 'E', 65-83 <LIU>  
A:Experimental source: brain, clone 8.1  
C:Superfamily: calreticulin  
C:Keywords: calcium binding; glycoprotein

F:397-400/Region: endoplasmic reticulum retention signal  
F:120-146/Disulfide bonds: #status experimental  
F:162/Binding site: carbohydrate (Asn) (covalent) #status experimental

Query Match 98.5%; Score 335; DB 2; Length 400;  
Best Local Similarity 98.4%; Pred. No. 1.7e-32;  
Matches 60; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TDMHGDSEYNIMFGPDICGPGTKKVVHIFNYKGNVLIINKDIRCKDDETHLYTLIVRPD 60  
|||||  
DB 103 TDMHGDSEYNIMFGPDICGPGTKKVVHIFNYKGNVLIINKDIRCKDDETHLYTLIVRPD 162

QY 61 N 61  
DB 163 N 163

RESULT 3  
S06763  
calreticulin precursor - mouse  
N:Alternate names: 55K calcium-binding reticuloplasmin; calregulin  
C:Species: Mus musculus (house mouse)  
C:Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 10-Sep-1999  
A:Accession: S06763; JCI444; PCI233; A57498  
R:Smith, M.J.; Koch, G.L.E.  
EMBO J. 8, 3581-3586, 1989  
A:Title: Multiple zones in the sequence of calreticulin (CRP55, calregulin, HACBP), a  
A:Reference number: S06763; MUID:90059955  
A:Accession: S06763  
A:Molecule type: DNA  
A:Residues: 1-416 <SMI>  
A:Cross-references: EMBL:X14926; NID:g50567; PIDN:CAA33053.1; PID:g50568  
R:Mazzarella, R.A.; Gold, P.; Cunningham, M.; Green, M.  
Gene 120, 217-225, 1992  
A:Title: Determination of the sequence of an expressible cDNA clone encoding Erp60/ca  
A:Reference number: JCI444; MUID:93013037  
A:Accession: JCI444  
A:Molecule type: mRNA  
A:Residues: 1-416 <MAZ>  
A:Cross-references: GB:M92988; NID:g193084; PIDN:AAA37569.1; PID:g193085  
A:Accession: PCI233  
A:Molecule type: protein  
A:Residues: 18-41 <MAZ>  
R:White, T.K.; Zhu, Q.; Tanzer, M.L.  
J. Biol. Chem. 270, 15926-15929, 1995  
A:Title: Cell surface calreticulin is a putative mannoside lectin which triggers mouse  
A:Reference number: A57498; MUID:95332280  
A:Accession: A57498  
A:Status: preliminary  
A:Molecule type: protein  
A:Residues: 74-80; 142-151; 186-193 <WHI>  
C:Superfamily: calreticulin  
C:Keywords: calcium binding  
F:1-17/Domain: signal sequence #status predicted <SIG>  
F:18-416/Product: calregulin #status experimental <MAT>  
F:413-416/Region: endoplasmic reticulum retention signal

Query Match 98.5%; Score 335; DB 1; Length 416;  
Best Local Similarity 100.0%; Pred. No. 1.8e-32;  
Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DMHGDSEYNIMFGPDICGPGTKKVVHIFNYKGNVLIINKDIRCKDDETHLYTLIVRPD 61  
|||||  
DB 121 DMHGDSEYNIMFGPDICGPGTKKVVHIFNYKGNVLIINKDIRCKDDETHLYTLIVRPD 180

RESULT 4  
JH0819  
calreticulin precursor - rat  
N:Alternate names: calcium-binding protein 3  
C:Species: Rattus norvegicus (Norway rat)

C:Date: 30-Sep-1993 #sequence\_revision 20-Aug-1994 #text\_change 20-Jun-2000  
C:Accession: JH0819; A49176; S11205; PC1109; S45036; S04867; S39372; A34473; S13045  
R:Nakamura, M.; Moriya, M.; Baba, T.; Michikawa, Y.; Yamanobe, T.; Arai, K.; Okinaga, S.  
Exp. Cell Res. 205, 101-110, 1993  
A:Title: An endoplasmic reticulum protein, calreticulin, is transported into the acrosom  
A:Reference number: A49176; MUID:93202172  
A:Accession: JH0819  
A:Molecule type: mRNA  
A:Residues: 1-416 <NAK>  
A:Cross-references: GB:D78308; NID:g1089798; PIDN:BAAL1345.1; PID:g1845572  
A:Accession: A49176  
A:Status: preliminary  
A:Molecule type: protein  
A:Residues: 1-416 <NAK>  
A:Cross-references: GB:D78308; NID:g1089798; PIDN:BAAL1345.1; PID:g1845572  
A:Experimental source: Sprague-Dawley, spermatogenic cells  
A:Note: sequence extracted from NCBI backbone (NCBIN:127639, NCBI:P:127643)  
R:Murthy, K.K.; Banville, D.; Srikanth, C.B.; Carrier, F.; Holmes, C.; Bell, A.; Patel, Y.  
Nucleic Acids Res. 18, 4933, 1990  
A:Title: Structural homology between the rat calreticulin gene product and the Onchocerc  
A:Reference number: S11205; MUID:90370496  
A:Accession: S11205  
A:Molecule type: mRNA  
A:Residues: 1-416 <NAK>  
A:Cross-references: EMBL:X53363; NID:g55854; PIDN:CAA37446.1; PID:g55855  
R:Nakamura, M.; Michikawa, Y.; Baba, T.; Okinaga, S.; Arai, K.  
Biochem. Biophys. Res. Commun. 186, 668-673, 1992  
A:Title: Calreticulin is present in the acrosome of spermatozoa of rat testis.  
A:Reference number: PC1109; MUID:92360010  
A:Accession: PC1109  
A:Molecule type: protein  
A:Residues: 18-32 <NAK2>  
A:Experimental source: testis, strain Sprague-Dawley  
R:Soennichsen, B.; Fuellekrug, J.; van Nguyen, P.; Diekmann, W.; Robinson, D.G.; Mieskes  
submitted to the EMBL Data Library, May 1994  
A:Description: Retention and retrieval: both mechanisms cooperate to maintain calreticul  
A:Reference number: S45036  
A:Accession: S45036  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-416 <SOE>  
A:Cross-references: EMBL:X79327; NID:g488840; PIDN:CAA55890.1; PID:g488841  
R:Lone, Y.C.; Bailey, A.; Latruffe, N.  
submitted to the EMBL Data Library, December 1988  
A:Reference number: S04867  
A:Accession: S04867  
A:Molecule type: mRNA  
A:Residues: 'R', 270-358, 'AAG' <LON>  
A:Cross-references: EMBL:X13702; NID:g56055; PIDN:CAA31987.1; PID:g930260  
A:Note: the authors designated the protein as D-beta-hydroxybutyrate dehydrogenase  
R:Yokoi, T.; Nagayama, S.; Kajiwara, R.; Kawaguchi, Y.; Horiuchi, R.; Kamataki, T.  
Biochim. Biophys. Acta 1158, 339-344, 1993  
A:Title: Identification of protein disulfide isomerase and calreticulin as autoimmune an  
A:Reference number: S39371; MUID:94072621  
A:Accession: S39372  
A:Molecule type: protein  
A:Residues: 18-23, 'X', 25-32 <YOK>  
R:Van, P.N.; Peter, F.; Soelling, H.D.  
J. Biol. Chem. 264, 17494-17501, 1989  
A:Title: Four intracisternal calcium-binding glycoproteins from rat liver microsomes wit  
itive calcium sequestering rat liver vesicles.  
A:Reference number: A34473; MUID:90008920  
A:Accession: A34473  
A:Status: preliminary  
A:Molecule type: protein  
A:Residues: 18-36 <VAN>  
R:Trevies, S.; de Mattei, M.; Lanfredi, M.; Villa, A.; Green, N.M.; MacLennan, D.H.; Melc  
Biochem. J. 271, 473-480, 1990  
A:Title: Calreticulin is a candidate for a calsequestrin-like function in Ca(2+)-storage  
A:Reference number: S13045; MUID:91054414  
A:Accession: S13045  
A:Molecule type: protein  
A:Residues: 18-29 <TRE>

C:Superfamily: calreticulin  
C:Keywords: calcium binding; glycoprotein  
F:1-17/Domain: signal sequence #status predicted <SIG>  
F:18-416/Product: calreticulin #status experimental <MAT>  
F:204-212/Region: nuclear location signal  
F:413-416/Region: endoplasmic reticulum retention signal  
F:344/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 98.5%; Score 335; DB 2; Length 416;  
Best Local Similarity 100.0%; Pred. No. 1.8e-32;  
Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 DMHGDSEYNIMFGPDICGPGTKKVHVIFNYGKNVLINIKDKDDETHLYTLIVRPDN 61  
|||||  
Db 121 DMHGDSEYNIMFGPDICGPGTKKVHVIFNYGKNVLINIKDKDDETHLYTLIVRPDN 180  
|||||

## RESULT 5

A34154  
calreticulin precursor, skeletal muscle - rabbit  
C:Species: Oryctolagus cuniculus (domestic rabbit)  
C:Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 10-Sep-1999  
C:Accession: A34154; S13047  
R:Fliegel, L.; Burns, K.; MacLennan, D.H.; Reithmeier, R.A.F.; Michalak, M.  
J. Biol. Chem. 264, 21522-21528, 1989  
A:Title: Molecular cloning of the high affinity calcium-binding protein (calreticulin  
A:Reference number: A34154; MUID:90094320  
A:Accession: A34154  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-418 <FLI>  
A:Cross-references: GB:J05138; NID:g164858; PIDN:AAA31188.1; PID:g164859  
R:Trevies, S.; de Mattei, M.; Lanfredi, M.; Villa, A.; Green, N.M.; MacLennan, D.H.; M  
Biochem. J. 271, 473-480, 1990  
A:Title: Calreticulin is a candidate for a calsequestrin-like function in Ca(2+)-stor  
A:Reference number: S13045; MUID:91054414  
A:Accession: S13047  
A:Molecule type: protein  
A:Residues: 19-32 <TRE>  
C:Superfamily: calreticulin  
C:Keywords: skeletal muscle  
F:1-17/Domain: signal sequence #status predicted <SIG>  
F:415-418/Region: endoplasmic reticulum retention signal

Query Match 98.5%; Score 335; DB 1; Length 418;  
Best Local Similarity 100.0%; Pred. No. 1.8e-32;  
Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 DMHGDSEYNIMFGPDICGPGTKKVHVIFNYGKNVLINIKDKDDETHLYTLIVRPDN 61  
|||||  
Db 121 DMHGDSEYNIMFGPDICGPGTKKVHVIFNYGKNVLINIKDKDDETHLYTLIVRPDN 180  
|||||

## RESULT 6

S36799  
calreticulin precursor, brain isoform 2 - bovine  
C:Species: Bos primigenius taurus (cattle)  
C:Date: 10-Dec-1993 #sequence\_revision 23-Mar-1995 #text\_change 13-Aug-1999  
C:Accession: S36799; S36800  
R:Liu, N.; Fine, R.E.; Johnson, R.J.  
Biochim. Biophys. Acta 1202, 70-76, 1993  
A:Title: Comparison of cDNAs from bovine brain coding for two isoforms of calreticuli  
A:Reference number: S36799; MUID:93385184  
A:Accession: S36799  
A:Molecule type: mRNA  
A:Residues: 1-421 <LIU>  
A:Cross-references: GB:LI13462; NID:g348693; PIDN:AAC37307.1; PID:g348694  
A:Experimental source: brain, clone 9.4  
A:Accession: S36800  
A:Molecule type: protein  
A:Residues: 35-45 <LI2>





C:Accession: S25851; T33996  
R:Smith, M.J.  
DNA Seq. 2, 235-240, 1992  
A:Title: A C. elegans gene encodes a protein homologous to mammalian calreticulin.  
A:Reference number: S25851; MUID:92339978  
A:Accession: S25851  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-395 <SM1>  
A:Cross-references: EMBL:X59589; NID:g6693; PIDN:CAA42159.1; PID:g6694  
R:Bauer, C.; Courtney, L.; Laplant, Y.  
submitted to the EMBL Data Library, February 1999  
A:Description: The sequence of C. elegans cosmid Y38A10A.  
A:Reference number: Z21453  
A:Accession: T33996  
A:Status: preliminary; translated from GB/EMBL/DBDJ  
A:Molecule type: DNA  
A:Residues: 1-395 <BAU>  
A:Cross-references: EMBL:AF125963; PIDN:AAU14746.1; GSPDB:GN00023; CESP:Y38A10A.5  
A:Experimental source: strain Bristol N2; clone Y38A10A  
C:Genetics:  
A:Gene: CESP:Y38A10A.5  
A:Map position: 5  
A:Introns: 107/3; 315/3  
C:Superfamily: calreticulin  
F:1-15/domain: signal sequence #status predicted <SIG>  
F:392-395/Region: endoplasmic reticulum retention signal

```
Query Match      68.7%; Score 233.5; DB 2; Length 395;
Blast Local Similarity 68.3%; Pred. No. 2.4e-20;
Matches 41; Conservative 8; Mismatches 10; Indels 1; Gaps 1;
```

```

RESULT 15
T14554
calreticulin - beet
C:Species: Beta vulgaris (beet)
C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Jun-2000
C:Accession: T14554
R:Viereck, R.
submitted to the EMBL Data Library, October 1997
A:Description: Nucleotide sequence from sugar beet calreticulin.
A:Reference number: Z18137
A:Accession: T14554
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: mRNA
A:Residues: 1-416 <VIEW>
A:Cross-references: EMBL:AJ002057
A:Experimental source: strain diploide Inzuchtlinie KWS; leaf
C:Superfamily: calreticulin
C:Keywords: calcium binding

```

```
Query Match      60.9%; Score 207; DB 2; Length 416;
Best Local Similarity 64.3%; Pred. No. 3.8e-17;
Matches 36; Conservative 7; Mismatches 13; Indels 0; Gaps 0;
```

Search completed: January 9, 2002, 15:02:02  
Job time: 189 sec

Result No.	Query			DB	ID	Description
	Score	Match	Length			
1	537	54.3	415	4	US-08-675-816-2	Sequence 2, Appli
2	290	29.9	593	1	US-08-296-362-2	Sequence 2, Appli
3	227.5	23.4	542	4	US-08-675-816-6	Sequence 6, Appli
4	89	9.2	660	4	US-09-181-706-8	Sequence 8, Appli
5	89	9.2	660	4	US-09-458-791-8	Sequence 8, Appli
6	89	9.2	660	4	US-09-459-066-8	Sequence 8, Appli
7	77.5	8.0	642	2	US-08-245-511-48	Sequence 48, Appli
8	77.5	8.0	642	2	US-08-600-993A-48	Sequence 48, Appli
9	77	7.9	15	3	US-08-946-026-53	Sequence 53, Appli
10	75	7.7	591	3	US-08-991-408-4	Sequence 4, Appli
11	75	7.7	1013	2	US-08-866-650-5	Sequence 5, Appli
12	75	7.7	1013	2	US-09-021-287-5	Sequence 5, Appli
13	75	7.7	1013	3	US-08-991-408-2	Sequence 2, Appli
14	75	7.7	1013	4	US-09-240-473-5	Sequence 5, Appli
15	72.5	7.5	1484	2	US-08-231-193A-56	Sequence 56, Appli
16	72.5	7.5	1484	2	US-08-486-273A-56	Sequence 56, Appli
17	72.5	7.5	1484	3	US-08-940-086A-56	Sequence 56, Appli
18	72	7.4	263	1	US-08-152-922A-5	Sequence 5, Appli
19	72	7.4	511	1	US-08-480-604A-20	Sequence 20, Appli
20	72	7.4	511	2	US-08-405-496A-20	Sequence 20, Appli
21	72	7.4	511	4	US-08-915-136-20	Sequence 20, Appli
22	72	7.4	608	1	US-08-480-604A-21	Sequence 21, Appli
23	72	7.4	608	2	US-08-405-496A-21	Sequence 21, Appli
24	72	7.4	608	4	US-08-915-136-21	Sequence 21, Appli
25	72	7.4	609	1	US-08-480-604A-30	Sequence 30, Appli
26	72	7.4	609	4	US-08-915-136-30	Sequence 30, Appli
27	72	7.4	984	1	US-08-257-073-3	Sequence 3, Appli

Db	79	S	A	S	E	P	E	F	S	N	K	D	T	L	V	F	Q	S	V	K	H	E	Q	L	D	C	G	G	Y	N	K	L	L	S	S	T	D	Q	K	F	G	G	D	T	P	S	I	M	F	G	P	D	I	C	138
Qy	121	G	P	C	T	K	K	V	H	V	I	N	F	N	K	G	N	V	L	I	N	K	D	I	R	C	K	D	E	F	T	H	L	I	V	R	P	D	T	I	E	V	K	I	D	N	S	O	V	E	S	G	L	179	
Db	139	G	Y	S	T	K	H	A	L	I	N	D	N	F	N	H	L	I	K	S	P	E	T	Q	L	T	H	V	T	V	I	R	P	A	T	I	S	I	L	D	I	N	E	K	O	T	G	S	L	197					

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RESULT      2
US-08-296-362-2
: Sequence 2, Application US/08296362
: Patent No. 5691306
: GENERAL INFORMATION:
: APPLICANT: Bergeron, John J.M.
: APPLICANT: Thomas, David Y.
: APPLICANT: Wada, Ikuro
: TITLE OF INVENTION: METHODS OF DETECTION AND TREATMENT OF
: TITLE OF INVENTION: PROTEIN TRAFFICKING DISORDERS AND INCREASING SECRETORY
: TITLE OF INVENTION: PROTEIN PRODUCTION
: NUMBER OF SEQUENCES: 2
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: SEED and BERRY
: STREET: 6300 Columbia Center, 701 Fifth Avenue
: CITY: Seattle
: STATE: Washington
: COUNTRY: US
: ZIP: 98104-7092
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patent In Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/296,362
: FILING DATE: 25-AUG-1994
: CLASSIFICATION: 435
: ATTORNEY/AGENT INFORMATION:
: NAME: Dethr, Manya S.
: REGISTRATION NUMBER: 37,120
: REFERENCE/DOCKET NUMBER: 690066.401C1
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (206) 622-4900
: TELEFAX: (206) 682-6031
: TELEX: 3723836
: INFORMATION FOR SEQ ID NO: 2:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 593 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
: MOLECULE TYPE: protein
US-08-296-362-2

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Query Match          29.98;   Score 290;   DB 1;   Length 593;
Best Local Similarity 38.18;   Pred. No. 2.1e-24;
Match@77; Conservative 26; Mismatches 65; Indels 34; Gaps 9;

QY      4 VYFKEQFLDGGWTSRWLESKKHSD----FGKFVLLSSCKFYGOEEK-----DKGLQTS 52
       ||| : | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      70 VYFADSF--DRGTUGSGLLSRAKAKDDTDDETAKY--DGKWEVDDEMKETKLPGDFKGLVM 124
       ||| : | | | | | | | | | | | | | | | | | | | | | | | | | | | |

QY     53 QDARFYALSASF-EFFSNKGQTLVVQFTVKRHEQNIDCGGYVKLFPN---SLQDTMHG 107
       ||| : | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db    125 SRAKHHAIASAKLNKPFLFDTKPLVQVEVNPNQTECGGAYVKLLSKTPNELNQD--FHD 182
       ||| : | | | | | | | | | | | | | | | | | | | | | | | | | | | |

QY    108 DSEYNIMFGPDICGPTKKVHVIVNYGKNVLINKDIRCK-----DDEFTHLYTL 157
       ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db    183 KTPYTIAFGPDKCE-DYKLFIERHNPKTGVTEEKHAKRPDADLKTYTFDCKKTHLYTL 241
       ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | |

QY    158 IVRPNDNTYEYKIDNSQVESGSL 179
       ||| : | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db   242 ILNPDSFEILVDQSIVNSGNL 263
       ||| : | | | | | | | | | | | | | | | | | | | | | | | | | | | |

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```

RESULT      3
US-08-675-816-6
; Sequence 6, Application US/08675816
; Patent No. 6171864
; GENERAL INFORMATION:
; APPLICANT: Coughlan, Sean J.
; APPLICANT: Winfrey, Jr., Ron J.
; TITLE OF INVENTION: CALRETICULIN AND CALNEXIN GENES AND PROMOTER REGIONS AND US
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Seed and Berry
; STREET: 701 Fifth Ave. Suite 6300
; CITY: Seattle
; STATE: Washington
; COUNTRY: U.S.A.
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/675,816
; FILING DATE: 05-JUL-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENCY INFORMATION:
; NAME: No. 6171864tenburg, Carol
; REGISTRATION NUMBER: 39,317
; REFERENCE/DOCKET NUMBER: 750027.401
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206-622-4500
; TELEFAX: (206)-682-6031
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 542 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-675-816-6

Query Match      23.4%; Score 227.5; DB 4; Length 542;
Best Local Similarity 36.0%; Pred. No. 2.2e-17;
Matches 64; Conservative 24; Mismatches 73; Indels 17; Gaps 10;

QY      6  FKQFLDGDGWTNRWIESKHKSDFGKFLVLSGGKFGYDEEMDKGLQTSQDARFYALSASF- 64
Db      35  FYESF--EDSFEGRWTLSA-KDDY-KGEWKHAKSEGHDE--YGLLYSEKARKYATVKELD 88
QY      65  EPTSNKGQTLVVGQFTVKHEQIDCGGGYVK-LFPNSLDQT--DMHGDSFYNIMFGPDICG 121
Db      89  EPATLKDGTVILQFETRFQNGLECGGAYLYLRPQEAQWPKDFDNDSPYSIMFGPDKCG 148
QY      122  PGTGKKVHVIENYKG--KNVLINKDIR----CKDEFTHLYTLVRPDNTVEVKIDNSQ 173
Db      149  -ATNKVHFILKHKNPKSGEYIEHHLKPPSPVPSDKLTHVYTAILKPDNEURLIVDGE 205

RESULT      4
US-09-181-706-8
; Sequence 8, Application US/09181706
; Patent No. 6130068
; GENERAL INFORMATION:
; APPLICANT: Melange K. Spriggs, Michael R. Comeau,
; APPLICANT: Robert F. DuBose, Richard S. Johnson
; TITLE OF INVENTION: VIRAL ENCODED SEMAPHORIN PROTEIN
; TITLE OF INVENTION: RECEPTOR DNA AND POLYPEPTIDES
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Janis C. Henry
; STREET: 51 University St.
; CITY: Seattle

```





;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/09/459,066  
;; FILING DATE:  
;; CLASSIFICATION:  
;; PRIOR APPLICATION DATA: 08/958,598  
;; FILING DATE:  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Henry, Janis C  
;; REGISTRATION NUMBER: 34,347  
;; REFERENCE/DOCKET NUMBER: 2631  
;; TELEPHONE: (206)470-4189  
;; TELEFAX: (206)233-0644  
;; INFORMATION FOR SEQ ID NO: 8:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 660 amino acids  
;; TYPE: amino acid  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: protein  
US-09-459-066-8

Query Match 9.2%; Score 89; DB 4; Length 660;  
Best Local Similarity 20.6%; Pred. No. 0.14;  
Matches 41; Conservative 25; Mismatches 91; Indels 42; Gaps 6;  
QY 5 YPKQPLDGDGWTNRWIESKHKSDECKFVLS---SKFYGDDEKOKGLQTSQDAREYALS 61  
DB 448 YIAQMCINDEGGPSS-LSSHRWSTFLKVELECDIDGRSYRQTIHKAIKTNDTILYVFF 506  
QY 62 ASFEPENKGGTLVQFTVKHQNDICGGYVKLPFNSLDQTDHMGDSEYNIMFGPDICG 121  
DB 507 DS--PYKSALCTYSNNAIKHSEFSKLGYYTKQLPSP-----APGICL 548  
QY 122 PTKKV-HYFN-----YKGNVLINKDIRCKDDFTHLTYLIVRP 161  
DB 549 PAKGVVPHFTFDIEQYNELDDIIRKPLSQPIEGSPGVKWFIDIKENEHREYRIVFIKE 608  
QY 162 DNTYEVKIDNSQVSGSLE 180  
DB 609 NTIYSFDTKSKQTRSAQVD 627

RESULT 7  
US-08-245-511-48  
; Sequence 48, Application US/08245511  
; Patent No. 5928900  
; GENERAL INFORMATION:  
; APPLICANT: Masure, H Robert  
; APPLICANT: Pearce, Barbara J  
; APPLICANT: Tuomanen, Elaine  
; TITLE OF INVENTION: BACTERIAL EXPORTED PROTEINS AND  
; NUMBER OF SEQUENCES: 58  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Klauber & Jackson  
; STREET: 411 Hackensack Avenue  
; CITY: Hackensack  
; STATE: New Jersey  
; COUNTRY: USA  
; ZIP: 07601  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent in Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/245,511  
; FILING DATE: 18-MAY-1994  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/116,541

;; FILING DATE: 01-SEP-1994  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Jackson Esq., David A.  
;; REGISTRATION NUMBER: 26,742  
;; REFERENCE/DOCKET NUMBER: 600-1-069 CIP  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: 201 487-5800  
;; TELEFAX: 201 343-1684  
;; TELEX: 133521  
;; INFORMATION FOR SEQ ID NO: 48:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 642 amino acids  
;; TYPE: amino acid  
;; TOPOLOGY: unknown  
;; MOLECULE TYPE: peptide  
;; HYPOTHETICAL: NO  
;; ANTI-SENSE: NO  
;; ORIGINAL SOURCE:  
;; ORGANISM: Streptococcus pneumoniae  
;; IMMEDIATE SOURCE:  
;; CLONE: am1A  
;; FEATURE:  
;; OTHER INFORMATION: NOTE: the reference contains a  
;; OTHER INFORMATION: sequence error; the correct sequence shown below is obtain  
;; OTHER INFORMATION: from GENBANK  
;; PUBLICATION INFORMATION:  
;; AUTHORS: Alloung, et al.  
;; JOURNAL: Mol. Microbiol.  
;; VOLUME: 4  
;; PAGES: 633-644  
;; DATE: 1990  
US-08-245-511-48  
Query Match 8.0%; Score 77.5; DB 2; Length 642;  
Best Local Similarity 21.2%; Pred. No. 2.6;  
Matches 42; Conservative 20; Mismatches 81; Indels 55; Gaps 8;  
QY 16 WTSR-----W-----IESKHKSDFGKFLVSSGKFGYDEKDKGLQTSQDARFYALSASF 64  
DB 164 WNSKLTYSIFWPLNEEFETSKGDFAKPTDPTSLLYNGPFLKGLTAKSSVEF----VKN 219  
QY 65 EPFSNKGOTLVVQFTVKH-----EQNIDCGG-GYVKLPFNSLDQT---DMHCDSEY 111  
DB 220 EQWDRKNVHLDITINLAYYDGDQESLERNTSGAYSARLYPTSSNYSKVAEYKDNLY 279  
QY 112 NIMFGPDICGPGTKKVHVIFNYKG-----KNVLINKDIR----- 145  
DB 280 YTGSGGIAGLGVNIDRQSYNTSKTTDSEKVTAKKALLINKDFRQALNFALDRSAYSQAI 339  
QY 146 -CKDDEFTHLYTLIVRPD 162  
DB 340 NGKDGAAALAVRNLFVKPD 357  
RESULT 8  
US-08-600-993A-48  
; Sequence 48, Application US/08600993A  
; Patent No. 5981229  
; GENERAL INFORMATION:  
; APPLICANT: Masure, H Robert  
; APPLICANT: Pearce, Barbara J  
; APPLICANT: Tuomanen, Elaine  
; TITLE OF INVENTION: BACTERIAL EXPORTED PROTEINS AND  
; NUMBER OF SEQUENCES: 59  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Klauber & Jackson  
; STREET: 411 Hackensack Avenue  
; CITY: Hackensack  
; STATE: New Jersey  
; COUNTRY: USA  
; ZIP: 07601

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/600.993A  
FILING DATE: 1-MAR-1996  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/245,511  
FILING DATE: 18-MAY-1994  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/116,541  
FILING DATE: 01-SEP-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Jackson Esq., David A.  
REGISTRATION NUMBER: 26,742  
REFERENCE/DOCKET NUMBER: 600-1-069 US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 201 487-5800  
TELEFAX: 201 343-1684  
TELEX: 133521  
INFORMATION FOR SEQ ID NO: 48:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 642 amino acids  
TYPE: amino acid  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
ORIGINAL SOURCE:  
ORGANISM: Streptococcus pneumoniae  
IMMEDIATE SOURCE:  
CLONE: amla  
FEATURE:  
OTHER INFORMATION: the reference contains a sequence error; the  
OTHER INFORMATION: correct sequence shown below is obtained from GENBANK  
PUBLICATION INFORMATION:  
AUTHORS: Alloing, et al.  
JOURNAL: Mol. Microbiol.  
VOLUME: 4  
PAGES: 633-644  
DATE: 1990  
US-08-600-993A-48

Query Match 8.0%; Score 77.5; DB 2; Length 642;  
Best Local Similarity 21.2%; Pred. No. 2.6;  
Matches 42; Conservative 20; Mismatches 81; Indels 55; Gaps 8;  
QY 16 WTSR-----W-----IESKHSDFGKFLVSSGKFGYDEKDKGLTSDQARFYALSASF 64  
DB 164 WNSKUTYSIFWPLNEEFETSGKDFAKPTDPTSLLYNGPFLKGLTAKSSVEF-----VKN 219  
QY 65 EFSNKGOTLVQVQTKH-----EONIDCGG-GYVKLFPNSLDQF---DMHGDSY 111  
DB 220 EYWKENVHLDTINLAYDGSQSLERNFTSGAYSARLYPTSSNYSKVAEYKDNLY 279  
QY 112 NFMFGPDICGPGTKKHVIFNYKG-----KNVINKDIR----- 145  
DB 280 YTGSGGIAGLVNIDRQSYNTSKTTDSKVKATKALLNKDFRQALNFDLRSAYSQAQI 339  
QY 146 -CKDDEFHLYTLVRPD 162  
DB 340 NGKDGAAALAVRNLFVKPD 357

RESULT 9  
US-08-946-026-53  
Sequence 53, Application US/089946026  
Patent No. 6034218

GENERAL INFORMATION:  
APPLICANT: Reed, Steven G.  
APPLICANT: Dillon, Davin C.  
APPLICANT: Twardzik, Daniel R.  
APPLICANT: Mitcham, Jennifer L.  
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR IMMUNOTHERAPY  
AND IMMUNODIAGNOSIS OF PROSTATE CANCER  
NUMBER OF SEQUENCES: 59  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: SEED and BERRY LLP  
STREET: 6300 Columbia Center, 701 Fifth Avenue  
CITY: Seattle  
STATE: Washington  
COUNTRY: USA  
ZIP: 98104-7092  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/946,026  
FILING DATE: 07-OCT-1997  
CLASSIFICATION: 424  
ATTORNEY/AGENT INFORMATION:  
NAME: Maki, David J.  
REGISTRATION NUMBER: 31,392  
REFERENCE/DOCKET NUMBER: 210121.424C1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (206) 622-4900  
TELEFAX: (206) 682-6031  
INFORMATION FOR SEQ ID NO: 53:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 15 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-946-026-53

Query Match 7.9%; Score 77; DB 3; Length 15;  
Best Local Similarity 100.0%; Pred. No. 0.013;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PAVYFKEQFLDGDG 15  
DB 2 PAVYFKEQFLDGDG 15

RESULT 10  
US-08-991-408-4  
Sequence 4, Application US/08991408  
Patent No. 6008017  
GENERAL INFORMATION:  
APPLICANT: ARLETH, ANTHONY J.  
APPLICANT: WILLETTTE, ROBERT N.  
APPLICANT: ELSHOURBAGY, NABIL A.  
APPLICANT: LI, XIAOTONG  
TITLE OF INVENTION: HUMAN CARDIAC/BRAIN TOLLOID-LIKE  
NUMBER OF SEQUENCES: 4  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: RATNER & PRESTIA  
STREET: P.O. BOX 980  
CITY: VALLEY FORGE  
STATE: PA  
COUNTRY: USA  
ZIP: 19482  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSEQ for Windows Version 2.0



APPLICANT: Greenspan, Daniel S

; SOFTWARE: PatentIn Release #1.0, Version #1.23

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; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/231.193A
; FILING DATE: 20-APR-1994
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/052,459
; FILING DATE: 20-APR-1993
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Seldman, Stephanie
; REGISTRATION NUMBER: 33,779
; REFERENCE/DOCKET NUMBER: 6362-9383
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-238-0999
; TELEFAX: 619-238-0062
; INFORMATION FOR SEQ ID NO: 56:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1484 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-231-193A-56

Query Match 7.5%; Score 72.5; DB 2; Length 1484;
Best Local Similarity 27.7%; Pred. No. 32;
Matches 23; Conservative 13; Mismatches 28; Indels 19; Gaps 4;

QY 45 KDKG--LQTSQDARFVALSASPEPFSNKGQTLVVQFTVKHEQNIDCGGYV---KLEPNS 99
      |||| : | : ||| | : | : | : | : | : | : | : | : | : | : | : | : | :
Db 1325 KDKGRPMGSPVAHMPESAGESTFANNKSSVP---TAGHHHHNNPPGGGYMLSKSLYPDR 1381

QY 100 L-----DQTDHMGDSEY 111
      : || : || : |
Db 1382 VTQNPFIPTFGDDQCLLGSKSY 1404
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Search completed: January 9, 2002, 14:59:42  
Job time: 69 sec

GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: January 9, 2002, 14:58:53 ; Search time 43.73 Seconds  
(without alignments)  
313.547 Million cell updates/sec

Title: US-09-828-000-3  
Perfect score: 971  
Sequence: 1 EPAYPKQFLDGDGWTSRW.....PDNTYEVKIDNSQVESGSLE 180  
Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues  
Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR\_68.\*  
1: pir1.\*  
2: pir2.\*  
3: pir3.\*  
4: pir4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	971	100.0	417	1 A37047	calreticulin precu
2	933	96.1	416	2 JH0819	calreticulin precu
3	931	95.9	418	1 A34154	calreticulin precu
4	930	95.8	400	2 S43376	calreticulin, brai
5	930	95.8	416	1 S06763	calreticulin precu
6	835	86.0	411	2 S29129	calreticulin precu
7	804	82.8	405	1 JH0795	calreticulin (clon
8	797	82.1	384	2 S29130	calreticulin precu
9	796	82.0	419	2 S71343	calreticulin homol
10	699	72.0	406	2 A56637	calreticulin precu
11	619.5	63.8	395	2 S25851	calreticulin precu
12	542.5	55.9	336	2 A32507	41K larval antigen
13	539	55.5	412	2 T05703	calreticulin - bar
14	539	55.5	415	2 T05705	calreticulin - bar
15	536	55.2	421	2 S58170	calreticulin precu
16	531	54.7	416	2 T14554	calreticulin - bee
17	527	54.3	415	2 T10172	calreticulin - cas
18	522.5	53.8	421	2 S36799	calreticulin precu
19	522	53.8	416	2 T16968	calreticulin call
20	517	53.2	389	2 T03691	calreticulin - com
21	512	52.7	425	2 C96605	calreticulin (Ctrl
22	510	52.5	444	2 H86224	hypothetical prote
23	496	51.1	393	1 A48573	calreticulin autoa
24	347	35.7	422	2 T07841	probable calreticu
25	293	30.2	591	2 B54354	calnexin precursor
26	290	29.9	591	2 C54354	calnexin precursor
27	290	29.9	592	2 I53260	calnexin - human
28	290	29.9	593	1 A37273	calnexin precursor
29	288	29.7	592	2 A46673	calnexin precursor

RESULT 1  
A37047  
calreticulin precursor - human  
N:Alternate names: 52K ribonucleoprotein autoantigen Ro/SS-A; 60K integrin-binding pr  
C:Species: Homo sapiens (man)  
C:Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 18-Feb-2000  
C:Accession: A42330; A37047; A46452; A28812; PH1525; A40346; S11475; T45075  
R:McCaulliffe, D.P.; Yang, Y.S.; Wilson, J.; Sontheimer, R.D.; Capra, J.D.  
J. Biol. Chem. 267, 2557-2562, 1992  
A:Title: The 5'-flanking region of the human calreticulin gene shares homology with t  
A:Reference number: A42330; MUID:92129342  
A:Accession: A42330  
A:Molecule type: DNA  
A:Residues: 1-417 <MC2>  
A:Note: sequence extracted from NCBI backbone (NCBIN:78537, NCBIP:78536)  
R:McCaulliffe, D.P.; Lux, F.A.; Lieu, T.S.; Sanz, I.; Hanke, J.; Newkirk, M.M.; Bachin  
J. Clin. Invest. 85, 1379-1391, 1990  
A:Title: Molecular cloning, expression, and chromosome 19 localization of a human Ro/  
A:Reference number: A37047; MUID:90237213  
A:Accession: A37047  
A:Molecule type: mRNA  
A:Residues: 1-417 <MC2>  
A:Cross-references: GB:M32294; NID:g337486; PIDN:AAA36582.1; PID:g337487  
A:Note: the authors translated the codon GTA for residue 349 as Tyr  
R:Rokeach, L.A.; Haselby, J.A.; Mellof, J.F.; Smeenk, R.J.; Unnasch, T.R.; Greene, B.  
J. Immunol. 147, 3031-3039, 1991  
A:Title: Characterization of the autoantigen calreticulin.  
A:Reference number: A46452; MUID:92013129  
A:Accession: A46452  
A:Molecule type: mRNA  
A:Residues: 1-417 <R0K>  
A:Cross-references: GB:M4739; NID:g179881; PIDN:AAA51916.1; PID:g179882  
A:Note: sequence extracted from NCBI backbone (NCBIN:60749, NCBIP:60750)  
R:Lieu, T.S.; Newkirk, M.M.; Capra, J.D.; Sontheimer, R.D.  
J. Clin. Invest. 82, 96-101, 1988  
A:Title: Molecular characterization of human Ro/SS-A antigen. Amino terminal sequence  
A:Reference number: A28812; MUID:88273610  
A:Accession: A28812  
A:Molecule type: protein  
A:Residues: 18-41 <LIE>  
A:Note: 18-Ala was also found  
R:Dupuis, M.; Schaefer, E.; Krause, K.H.; Tschopp, J.  
J. Exp. Med. 177, 1-7, 1993  
A:Title: The calcium-binding protein calreticulin is a major constituent of lytic gra  
A:Reference number: PH1525; MUID:93115648  
A:Accession: PH1525  
A:Molecule type: protein  
A:Residues: 18-27 <DUP>  
A:Experimental source: LAK cell  
R:Roijani, M.V.; Finlay, B.B.; Gray, V.; Dedhar, S.  
Biochemistry 30, 9859-9866, 1991  
A:Title: In vitro interaction of a polypeptide homologous to human Ro/SS-A antigen (c

## ALIGNMENTS

A:Reference number: A40346; MUID:92002034  
A:Accession: A40346  
A:Molecule type: protein  
A:Residues: 18-34; R' <ROI>  
R:Krause, K.H.; Simmerman, H.K.B.; Jones, L.R.; Campbell, K.P.  
Biochem. J. 270, 545-548, 1990  
A:Title: Sequence similarity of calreticulin with a Ca(2+)-binding protein that co-purifies with the Golgi apparatus  
A:Reference number: S11475; MUID:90380058  
A:Accession: S11475  
A:Molecule type: protein  
A:Residues: 18-32 <KRA>  
R:Ramirez, M.; Carrano, A.  
submitted to the EMBL Data Library, November 1996  
A:Description: Characterization by genomic sequence analysis of a gene-rich 111 kb region  
A:Reference number: Z22906  
A:Accession: T45075  
A>Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-417 <LAW>  
A:Cross-references: EMBL:AD000092; PIDN:AA851176.1  
A:Experimental source: cell line 5H2-B; fibroblast  
C:Comment: Autoantibodies specific for this protein are found in Sjogren's syndrome and Sjogren's syndrome  
C:Graphics:  
A:Gene: GDB:CALR  
A:Cross-references: GDB:125179; OMIM:109091  
A:Map position: 19p13.3-19p13.2  
A:Introns: 41/1; 65/1; 133/1; 164/3; 272/3; 320/3; 351/3  
A:Note: CRT  
C:Superfamily: calreticulin  
C:Keywords: calcium binding; integrin binding  
F:1-17/Domain: signal sequence #status predicted <SIG>  
F:18-417/Product: calreticulin #status predicted <MAT>  
F:414-417/Region: endoplasmic reticulum retention signal

Query Match 100.0%; Score 971; DB 1; Length 417;  
Best Local Similarity 100.0%; Pred. No. 3.3e-80;  
Matches 180; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EPVAVFKQFLDGDGWTNRWIESKHKSDFGKFLVSSGKPYGDEKDKGLQTSQDARFYAL 60  
|||||  
DB 18 EPVAVFKQFLDGDGWTNRWIESKHKSDFGKFLVSSGKPYGDEKDKGLQTSQDARFYAL 77  
|||||

QY 61 SASFPFSNKGQTLVVOFTVKHEQNDICGGYVKLFPNSLDQTDHGDSEYNIMFGPDIC 120  
|||||  
DB 78 SASFPFSNKGQTLVVOFTVKHEQNDICGGYVKLFPNSLDQTDHGDSEYNIMFGPDIC 137  
|||||

QY 121 GPCTKKVHVIFNFKGNVLINIRCKDEFTHLVTLIVRPNTVEVKIDNSQVSGSLE 180  
|||||  
DB 138 GPCTKKVHVIFNFKGNVLINIRCKDEFTHLVTLIVRPNTVEVKIDNSQVSGSLE 197  
|||||

RESULT 2  
JH0819  
calreticulin precursor - rat  
N:Alternate names: calcium-binding protein 3  
C:Species: Rattus norvegicus (Norway rat)  
C:Date: 30-Sep-1993 #sequence\_revision 20-Aug-1994 #text\_change 20-Jun-2000  
C:Accession: JH0819; A49176; S11205; S45036; S04867; S39372; A34473; S13045  
R:Nakamura, M.; Moriya, M.; Baba, T.; Michikawa, Y.; Yamanobe, T.; Arai, K.; Okinaga, S.  
Exp. Cell Res. 205, 101-110, 1993  
A:Title: An endoplasmic reticulum protein, calreticulin, is transported into the acrosome  
A:Reference number: A49176; MUID:93202172  
A:Accession: JH0819  
A:Molecule type: mRNA  
A:Residues: 1-416 <NAK>  
A:Cross-references: GB:D78308; NID:g1089798; PIDN:BA11345.1; PID:g1845572  
A:Accession: A49176  
A>Status: preliminary  
A:Molecule type: protein  
A:Residues: 1-416 <NAK>  
A:Cross-references: GB:D78308; NID:g1089798; PIDN:BA11345.1; PID:g1845572  
A:Experimental source: Sprague-Dawley, spermatogenic cells

A:Note: sequence extracted from NCBI backbone (NCBIN:127639, NCBIPI:127643)  
R:Murthy, K.K.; Banville, D.; Srikant, C.B.; Carrier, F.; Holmes, C.; Bell, A.; Patel  
Nucleic Acids Res. 18, 4933, 1990  
A:Title: Structural homology between the rat calreticulin gene product and the Onchoc  
A:Reference number: S11205; MUID:90370496  
A:Accession: S11205  
A:Molecule type: mRNA  
A:Residues: 1-416 <MUR>  
A:Cross-references: EMBL:X53363; NID:g55854; PIDN:CAA37446.1; PID:g55855  
R:Nakamura, M.; Michikawa, Y.; Baba, T.; Okinaga, S.; Arai, K.  
Biochem. Biophys. Res. Commun. 186, 668-673, 1992  
A:Title: Calreticulin is present in the acrosome of spermatids of rat testis.  
A:Reference number: PC1109; MUID:92360010  
A:Accession: PC1109  
A:Molecule type: protein  
A:Residues: 18-32 <NAK2>  
A:Experimental source: testis, strain Sprague-Dawley  
R:Soennichsen, B.; Fuellekrug, J.; van Nguyen, P.; Diekmann, W.; Robinson, D.G.; Mies  
submitted to the EMBL Data Library, May 1994  
A:Description: Retention and retrieval: both mechanisms cooperate to maintain calreti  
A:Reference number: S45036  
A:Accession: S45036  
A>Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-416 <SOF>  
A:Cross-references: EMBL:X79327; NID:g488840; PIDN:CAA55890.1; PID:g488841  
R:Lone, Y.C.; Bailly, A.; Latruffe, N.  
submitted to the EMBL Data Library, December 1988  
A:Reference number: S04867  
A:Accession: S04867  
A:Molecule type: mRNA  
A:Residues: 18-358; 'AAG', 'AAG' <LON>  
A:Cross-references: EMBL:X13702; NID:g56055; PIDN:CAA31987.1; PID:g930260  
A:Note: the authors designated the protein as D-beta-hydroxybutyrate dehydrogenase  
R:Yokoi, T.; Nagayama, S.; Kajiwara, R.; Kawaguchi, Y.; Horiuchi, R.; Kamataki, T.  
Biochim. Biophys. Acta 1158, 339-344, 1993  
A:Title: Identification of protein disulfide isomerase and calreticulin as autoimmune  
A:Reference number: S39371; MUID:94072621  
A:Accession: S39371  
A:Molecule type: protein  
A:Residues: 18-23; 'X', '25-32' <YOK>  
R:Van, P.N.; Peter, F.; Soeling, H.D.  
J. Biol. Chem. 264, 17494-17501, 1989  
A:Title: Four intracisternal calcium-binding glycoproteins from rat liver microsomes  
A:Reference number: A34473; MUID:90008920  
A:Accession: A34473  
A>Status: preliminary  
A:Molecule type: protein  
A:Residues: 18-36 <VAN>  
R:Treves, S.; de Mattei, M.; Lanfredi, M.; Villa, A.; Green, N.M.; MacLennan, D.H.; M  
Biochem. J. 271, 473-480, 1990  
A:Title: Calreticulin is a candidate for a calsequestrin-like function in Ca(2+)-stor  
A:Reference number: S13045; MUID:91054414  
A:Accession: S13045  
A:Molecule type: protein  
A:Residues: 18-29 <TRE>  
C:Superfamily: calreticulin  
C:Keywords: calcium binding; glycoprotein  
F:1-17/Domain: signal sequence #status predicted <SIG>  
F:18-416/Product: calreticulin #status experimental <MAT>  
F:204-212/Region: nuclear location signal  
F:413-416/Region: endoplasmic reticulum retention signal  
F:344/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 96.1%; Score 933; DB 2; Length 416;  
Best Local Similarity 94.4%; Pred. No. 8.8e-77;  
Matches 170; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

QY 1 EPVAVFKQFLDGDGWTNRWIESKHKSDFGKFLVSSGKPYGDEKDKGLQTSQDARFYAL 60  
|||||  
DB 18 DPVAVFKQFLDGDGWTNRWIESKHKSDFGKFLVSSGKPYGDEKDKGLQTSQDARFYAL 77  
|||||



QY 61 SASFEPPSNKGTLLVQVFTVKHEQNIDCGGKVLFPNSLDQTMHGDSEYNIMFGPDIC 120  
 |||||||  
 Db 78 SARFEPFSNKGQTLVVQFTVKHEQNIDCGGKVLFPNSLDQTMHGDSEYNIMFGPDIC 137  
 |||||||  
 QY 121 GPGTKKVHVIFNYKGNVNLINKIRCKDDETHLYTLIVRPNTYEVKIDNSQVSGSLE 180  
 |||||||  
 Db 138 GPGTKKVHVIFNYKGNVNLINKIRCKDDETHLYTLIVRPNTYEVKIDNSQVSGSLE 197  
 |||||||

RESULT 3  
 A34154  
 calreticulin precursor, skeletal muscle - rabbit  
 C:Species: Oryctolagus cuniculus (domestic rabbit)  
 C:Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 10-Sep-1999  
 C:Accession: A34154; S13047  
 R:Fliegel, L.; Burns, K.; MacLennan, D.H.; Reithmeier, R.A.F.; Michalak, M.  
 J. Biol. Chem. 264, 21522-21528, 1989  
 A:Title: Molecular cloning of the high affinity calcium-binding protein (calreticulin) cDNA  
 A:Reference number: A34154; MUID:90094320  
 A:Status: preliminary  
 A:Accession: A34154  
 A:Molecule type: mRNA  
 A:Residues: 1-418 <FLI>  
 A:Cross-references: GB:J05138; NID:g164858; PIDN:AAA31188.1; PID:g164859  
 R:Treves, S.; de Mattei, M.; Lanfiredi, M.; Villa, A.; Green, N.M.; MacLennan, D.H.; Melchiorri, D.  
 Biochem. J. 271, 473-480, 1990  
 A:Title: Calreticulin is a candidate for a calsequestrin-like function in Ca(2+)-storage  
 A:Reference number: S13045; MUID:91054414  
 A:Accession: S13047  
 A:Molecule type: protein  
 A:Residues: 19-32 <TR>  
 C:Superfamily: calreticulin  
 C:Keywords: skeletal muscle  
 F:1-17/Domain: signal sequence #status predicted <SIG>  
 F:415-418/Region: endoplasmic reticulum retention signal

Query Match 95.9%; Score 931; DB 1; Length 418;  
 Best Local Similarity 95.6%; Pred. No. 1.3e-76;  
 Matches 172; Conservative 1; Mismatches 7; Indels 0; Gaps 0;

QY 1 EPAVVFKEQFLDGDGWTSRWIESKHSKDFGKFLVSSGKFGYGDDEKDKGLQTSQDARFYAL 60  
 |||||||  
 Db 18 EPVVFKEQFLDGDGWTSRWIESKHSKDFGKFLVSSGKFGYGDDEKDKGLQTSQDARFYAL 77  
 |||||||

QY 61 SASFEPPSNKGTLLVQVFTVKHEQNIDCGGKVLFPNSLDQTMHGDSEYNIMFGPDIC 120  
 |||||||  
 Db 78 SARFEPFSNKGQTLVVQVFTVKHEQNIDCGGKVLFPNSLDQTMHGDSEYNIMFGPDIC 137  
 |||||||

QY 121 GPGTKKVHVIFNYKGNVNLINKIRCKDDETHLYTLIVRPNTYEVKIDNSQVSGSLE 180  
 |||||||  
 Db 138 GPGTKKVHVIFNYKGNVNLINKIRCKDDETHLYTLIVRPNTYEVKIDNSQVSGSLE 197  
 |||||||

RESULT 4  
 S43376  
 calreticulin, brain isoform 1 - bovine  
 C:Species: Bos primigenius taurus (cattle)  
 C:Date: 20-Oct-1994 #sequence\_revision 23-Mar-1995 #text\_change 07-May-1999  
 C:Accession: S43376; S36801  
 R:Matsuoka, K.; Seta, K.; Yamakawa, Y.; Okuyama, T.; Shinoda, T.; Isobe, T.  
 Biochem. J. 298, 435-442, 1994  
 A:Title: Covalent structure of bovine brain calreticulin.  
 A:Reference number: S43376; MUID:94183174  
 A:Accession: S43376  
 A:Molecule type: protein  
 A:Residues: 1-400 <MAT>  
 A:Experimental source: brain  
 R:Liu, N.; Fine, R.E.; Johnson, R.J.  
 Biochim. Biophys. Acta 1202, 70-76, 1993  
 A:Title: Comparison of cDNAs from bovine brain coding for two isoforms of calreticulin.  
 A:Reference number: S36799; MUID:93385184

A:Accession: S36801  
 A:Status: nucleic acid sequence not shown  
 A:Molecule type: mRNA  
 A:Residues: 45-63, 'E', 65-83 <LIU>  
 A:Experimental source: brain, clone 8.1  
 C:Superfamily: calreticulin  
 C:Keywords: calcium binding; glycoprotein  
 F:397-400/Region: endoplasmic reticulum retention signal  
 F:120-146/Disulfide bonds: #status experimental  
 F:162/Binding site: carbohydrate (Asn) (covalent) #status experimental

Query Match 95.8%; Score 930; DB 2; Length 400;  
 Best Local Similarity 95.0%; Pred. No. 1.6e-76;  
 Matches 171; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY 1 EPAVVFKEQFLDGDGWTSRWIESKHSKDFGKFLVSSGKFGYGDDEKDKGLQTSQDARFYAL 60  
 :|||||  
 Db 1 DPTVFKEQFLDGDGWTSRWIESKHSKDFGKFLVSSGKFGYGDDEKDKGLQTSQDARFYAL 60  
 :|||||

QY 61 SASFEPPSNKGTLLVQVFTVKHEQNIDCGGKVLFPNSLDQTMHGDSEYNIMFGPDIC 120  
 |||||||  
 Db 61 SARFEPFSNKGQTLVVQVFTVKHEQNIDCGGKVLFPNSLDQTMHGDSEYNIMFGPDIC 120  
 |||||||

QY 121 GPGTKKVHVIFNYKGNVNLINKIRCKDDETHLYTLIVRPNTYEVKIDNSQVSGSLE 180  
 |||||||  
 Db 121 GPGTKKVHVIFNYKGNVNLINKIRCKDDETHLYTLIVRPNTYEVKIDNSQVSGSLE 180  
 |||||||

RESULT 5  
 S06763  
 calreticulin precursor - mouse  
 N:Alternate names: 55K calcium-binding reticuloplasmin; calregulin  
 C:Species: Mus musculus (house mouse)  
 C:Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 10-Sep-1999  
 C:Accession: S06763; JCI444; PC1233; A57498  
 R:Smith, M.J.; Koch, G.L.E.  
 EMBO J. 8, 3581-3586, 1989  
 A:Title: Multiple zones in the sequence of calreticulin (CRP55, calregulin, HACBP), a  
 A:Reference number: S06763; MUID:90059955  
 A:Accession: S06763  
 A:Molecule type: DNA  
 A:Residues: 1-416 <SMI>  
 A:Cross-references: EMBL:X14926; NID:g50567; PIDN:CAA33053.1; PID:g50568  
 R:Mazarella, R.A.; Gold, P.; Cunningham, M.; Green, M.  
 Gene 120, 217-225, 1992  
 A:Title: Determination of the sequence of an expressible cDNA clone encoding Erp60/ca  
 A:Reference number: JCI444; MUID:93013037  
 A:Accession: JCI444  
 A:Molecule type: mRNA  
 A:Residues: 1-416 <MAZ>  
 A:Cross-references: GB:M92988; NID:g193084; PIDN:AAA37569.1; PID:g193085  
 A:Accession: PC1233  
 A:Molecule type: protein  
 A:Residues: 18-41 <MAZ>  
 R:White, T.K.; Zhu, Q.; Tanzer, M.L.  
 J. Biol. Chem. 270, 15926-15929, 1995  
 A:Title: Cell surface calreticulin is a putative mannose lectin which triggers mous  
 A:Reference number: A57498; MUID:95332280  
 A:Accession: A57498  
 A:Status: preliminary  
 A:Molecule type: protein  
 A:Residues: 74-80;142-151;186-193 <WHI>  
 C:Superfamily: calreticulin  
 C:Keywords: calcium binding  
 F:1-17/Domain: signal sequence #status predicted <SIG>  
 F:18-416/Product: calregulin #status experimental <MAT>  
 F:413-416/Region: endoplasmic reticulum retention signal

Query Match 95.8%; Score 930; DB 1; Length 416;  
 Best Local Similarity 94.4%; Pred. No. 1.6e-76;  
 Matches 170; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

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QY 1 EPAVYKQFLDGDGWTSMWESKHKSDGKFLVSSGKFGYDEEDKGLQTSQDARFYAL 60
  :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 18 DPATYKQFLDGDGWTSMWESKHKSDGKFLVSSGKFGYDEEDKGLQTSQDARFYAL 77
  :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 61 SASPEFSSKNGQTLVVQFTVKHEQNDICGGYVKFLFPNSLDQTDHMGDSEYNIMFGPDIC 120
  :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 78 SAKFPEFSSKNGQTLVVQFTVKHEQNDICGGYVKFLFPNSLDQTDHMGDSEYNIMFGPDIC 137
  :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 121 GPCTKKVHVIFNYKGNKVLNIDCKDDKDEFTHLTYTLIVRPNTYEVKIDNSQVSGSLE 180
  :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 138 GPCTKKVHVIFNYKGNKVLNIDCKDDKDEFTHLTYTLIVRPNTYEVKIDNSQVSGSLE 197
  :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
RESULT 6
S29129
C:Species: Xenopus laevis (African clawed frog)
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 13-Aug-1999
C:Accession: S29129
R:Trevies, S.; Zorzato, F.; Pozzan, T.
Biochem. J. 287, 579-581, 1992
A:Title: Identification of calreticulin isoforms in the central nervous system.
A:Reference number: S29129; MUID:93074997
A:Accession: S29129
A:Molecule type: mRNA
A:Residues: 1-411 <TRE>
A:Cross-references: EMBL:X67597; NID:g64608; PIDN:CAA47866.1; PID:g64609
C:Superfamily: calreticulin
C:Keywords: glycoprotein
F:1-12/Domain: signal sequence (fragment) #status predicted <SIG>
F:13-411/Product: calreticulin #status predicted <MAT>
F:408-411/Region: endoplasmic reticulum retention signal
F:339/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 86.0%; Score 835; DB 2; Length 411;
Best Local Similarity 83.9%; Pred. No. 6.2e-68;
Matches 151; Conservative 15; Mismatches 14; Indels 0; Gaps 0;

QY 1 EPAVYKQFLDGDGWTSMWESKHKSDGKFLVSSGKFGYDEEDKGLQTSQDARFYAL 60
  :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 13 EPAVYKQFLDGDGWTSMWESKHKSDGKFLVSSGKFGYDEEDKGLQTSQDARFYAM 72
  :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 61 SASPEFSSKNGQTLVVQFTVKHEQNDICGGYVKFLFPNSLDQTDHMGDSEYNIMFGPDIC 120
  :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 73 SSFPEFSSKNGQTLVVQFTVKHEQNDICGGYVKFLFPNSLDQTDHMGDSEYNIMFGPDIC 132
  :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 121 GPCTKKVHVIFNYKGNKVLNIDCKDDKDEFTHLTYTLIVRPNTYEVKIDNSQVSGSLE 180
  :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 133 GPPTKKVHVIFNYKGNKVLNIDCKDDKDEFTHLTYTLIVRPNTYEVKIDNSQVSGSLE 192
  :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
RESULT 7
JH0795
calreticulin precursor - California sea hare
N:Alternate names: protein 407
C:Species: Aplysia californica (California sea hare)
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C:Accession: JH0795; B31409; F60977
R:Kennedy, T.E.; Kuhl, D.; Barzilai, A.; Sweatt, J.D.; Kandel, E.R.
Neuron 9, 1013-1024, 1992
A:Title: Long-term sensitization training in aplysia leads to an increase in calreticulin
A:Reference number: JH0795; MUID:93098937
A:Accession: JH0795
A:Molecule type: mRNA
A:Residues: 1-405 <KNS>
A:Cross-references: GB:S51239; NID:g262053; PIDN:AAB24569.1; PID:g262054
A:Experimental source: abdominal ganglion and antral nervous system
R:Kennedy, T.E.; Gawinowicz, M.A.; Barzilai, A.; Kandel, E.R.; Sweatt, J.D.
Proc. Natl. Acad. Sci. U.S.A. 85, 7008-7012, 1988
A:Title: Sequencing of proteins from two-dimensional gels by using in situ digestion and
tion in Aplysia.

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A:Reference number: A94207; MUID:88320566
A:Accession: B31409
A:Molecule type: protein
A:Residues: 'X',17-28,'X',30-31 <KE2>
R:Sweatt, J.D.; Kennedy, T.E.; Wager-Smith, K.; Gawinowicz, M.A.; Barzilai, A.; Karl,
Electrophoresis 10, 152-157, 1989
A:Title: Development of a database of amino acid sequences for proteins identified an
A:Reference number: A60977; MUID:89276264
A:Accession: F60977
A:Molecule type: protein
A:Residues: 'X',17-28,'X',30-31 <SWE>
C:Superfamily: calreticulin
C:Keywords: calcium binding; endoplasmic reticulum
F:1-15/Domain: signal sequence #status predicted <SIG>
F:16-405/Product: calreticulin #status experimental <MAT>
F:402-405/Region: endoplasmic reticulum retention signal

Query Match 82.8%; Score 804; DB 1; Length 405;
Best Local Similarity 79.4%; Pred. No. 3.9e-65;
Matches 143; Conservative 18; Mismatches 17; Indels 2; Gaps 1;

QY 1 EPAVYKQFLDGDGWTSMWESKHKSDGKFLVSSGKFGYDEEDKGLQTSQDARFYAL 60
  :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 16 DPTVYKQFLDGDGWTSMWESKHKSDGKFLVSSGKFGYDEEDKGLQTSQDARFYAL 73
  :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 61 SASPEFSSKNGQTLVVQFTVKHEQNDICGGYVKFLFPNSLDQTDHMGDSEYNIMFGPDIC 120
  :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 74 SAKFPEFSSKNGQTLVVQFTVKHEQNDICGGYVKFLFPNSLDQTDHMGDSEYNIMFGPDIC 133
  :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 121 GPCTKKVHVIFNYKGNKVLNIDCKDDKDEFTHLTYTLIVRPNTYEVKIDNSQVSGSLE 180
  :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 134 GPCTKKVHVIFNYKGNKVLNIDCKDDKDEFTHLTYTLIVRPNTYEVKIDNSQVSGSLE 193
  :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
RESULT 8
S29130
calreticulin (clone 8) - African clawed frog (fragment)
C:Species: Xenopus laevis (African clawed frog)
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 13-Aug-1999
C:Accession: S29130; T01068
R:Trevies, S.; Zorzato, F.; Pozzan, T.
Biochem. J. 287, 579-581, 1992
A:Title: Identification of calreticulin isoforms in the central nervous system.
A:Reference number: S29129; MUID:93074997
A:Accession: S29130
A:Molecule type: mRNA
A:Residues: 1-384 <TRE>
A:Cross-references: EMBL:X67598
A:Accession: T01068
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-339,'XTGR' <TRW>
A:Cross-references: EMBL:X67598; NID:g64610; PIDN:CAA47867.1; PID:g64611
A:Experimental source: CNS
C:Superfamily: calreticulin
C:Keywords: glycoprotein
F:381-384/Region: endoplasmic reticulum retention signal
F:316/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 82.1%; Score 797; DB 2; Length 384;
Best Local Similarity 85.2%; Pred. No. 1.6e-64;
Matches 144; Conservative 12; Mismatches 13; Indels 0; Gaps 0;

QY 12 DGDGWTSMWESKHKSDGKFLVSSGKFGYDEEDKGLQTSQDARFYALSAPFESNKG 71
  :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 1 DGDGWTSMWESKHKSDGKFLVSSGKFGYDEEDKGLQTSQDARFYAMSSRFESNKG 60
  :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 72 QTLVQFTVKHEQNDICGGYVKFLFPNSLDQTDHMGDSEYNIMFGPDICGCTKKVHVIF 131
  :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 61 QTLVQFTVKHEQNDICGGYVKFLFPNSLDQTDHMGDSEYNIMFGPDICGCTKKVHVIF 120
  :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

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A; Introns: 65/1; 222/3  
C; Superfamily: calreticulin  
C; Keywords: calcium binding; endoplasmic reticulum  
F; 1-17/Domain: signal sequence #status predicted <SIG>  
F; 403-406/Region: endoplasmic reticulum retention signal

Query Match                72.0%; Score 699; DB 2; Length 406;  
Best Local Similarity     74.2%; Pred. No. 1.2e-55;  
Matches      132; Conservative      14; Mismatches      30; Indels          2; Gaps          2;

QY      4   VYRKEQLDGDGWTSRWIESKHK-SDFGKFVLSGGKFYGDEEKDKGLQTSDARFYALS A 62  
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
DB      21   VLKENP-DNENWDETWIYSKHPKGEKGFLVTGTFFYNDAEADKGIOTSDARFYAAS R 79  
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
  
QY      63   SFEPSNKGTLLVVOFTVKHEQNIDCGGGYVKLPFNSLDQTDHMGDSYNTIMFGPDICGP I 122  
| : | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |  
DB      80   KFDGFSEDPPLVVQVSFKHEQNIDCGGGYVKLFDCLSDQTDHMGESPYEIMFGPDICGP L 139  
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
  
QY      123   GTKKVHVIFNYKGNVLINKDIRCKDDDEFTHLYTLIVRPDNTYEYKINDSQVESGSLE I 180  
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |  
DB      140   GTRKVHVIFS YKGNHLISKDIRCKDDVYTFHYTLIVRPDNTYEVLIDNEKVESGNLE I 197  
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

RESULT    11  
S25851  
calreticulin precursor - Caenorhabditis elegans  
C; Species: Caenorhabditis elegans  
C; Date: 06-Jan-1994 #sequence\_revision 10-Nov-1995 #text\_change 05-Nov-1999  
C; Accession: S25851; T33996  
R; Smith, M.J.  
DNA Seq. 2, 235-240, 1992  
A; Title: A C. elegans gene encodes a protein homologous to mammalian calreticulin.  
A; Reference number: S25851; MUID: 92329978  
A; Accession: S25851  
A; Status: preliminary  
A; Molecule type: DNA  
A; Residues: 1-395 <SMI>  
A; Cross-references: EMBL:X59589; NID:g6693; PIDN:CAA42159.1; PID:g6694  
R; Bauer, C.; Courtney, L.; Laplant, Y.  
submitted to The EMBL Data Library, February 1999  
A; Description: The sequence of C. elegans cosmid Y38A10A.  
A; Reference number: Z21453  
A; Accession: T33996  
A; Status: preliminary; translated from GB/EMBL/DDBJ  
A; Molecule type: DNA  
A; Residues: 1-395 <BAU>  
A; Cross-references: EMBL:AF125963; PIDN:RAD14746.1; GSPDB:GN00023; CESP:Y38A10A.5  
A; Experimental source: strain Bristol N2; clone Y38A10A  
C; Genetics:  
A; Gene: CESP:Y38A10A.5  
A; Map position: 5  
A; Introns: 107/3; 315/3  
C; Superfamily: calreticulin  
F; 1-15/Domain: signal sequence #status predicted <SIG>  
F; 392-395/Region: endoplasmic reticulum retention signal

Query Match                63.8%; Score 619.5; DB 2; Length 395;  
Best Local Similarity     63.5%; Pred. No. 1.8e-46;  
Matches      113; Conservative      26; Mismatches      36; Indels          3; Gaps          3;

QY      4   VYRKEQLDGDGWTSRWIESKHKSFGRVFSSGGKFYGDEEKDKGLQTSDARFYALS A 63  
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
DB      17   VFKEEFND-A-SWEKRWWQSXKHKDDFGAKLSACKFFDVESRDQGIIOTSQAIFYISRAK R 75  
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
  
QY      64   FE-PFSNKGQTLVVQFTVKHEQNIDCGGGYVKLPFNSLDQTDHMGDSYNTIMFGPDICGP I 122  
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |  
DB      76   FDXDFSNGKRTLVIOYTVKHEQIDCGGGYVKVMRADLDGDFHCGETPTYNMFGPDICGP L 135  
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
  
QY      123   GTKKVHVIFNYKGNVLINKDIRCKDDDEFTHLYTLIVRPDNTYEYKINDSQVESGSLE I 180  
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |  
DB      136   -TRRVHILNYKGNKLTKKETCKSDLTHTYLTIILNSDNTIEYVKIDGESAQTSGLE I 192  
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |



Query Match 55.2%; Score 536; DB 2; Length 421;  
Best Local Similarity 56.4%; Pred. No. 6.7e-41;  
Matches 101; Conservative 31; Mismatches 41; Indels 6; Gaps 3;  
Qy 4 VYKQFLDGDGTSRWTESKHSD--FGKFVLSGKFYGDDEKDKLOTSDARFYAL 60  
Db 27 VFFQKFF--EDGWESRWVKSWKDENWAGENNHTSGRWNGDAE--DKGIQTSEDYRFYAI 83  
Qy 61 SASPEPFSNKGQTLVVOFTVRKHEQNIDCGGYVKLFPPNSLDQTMHGDSEYNIMEGPDIC 120  
Db 84 SAEYPEFSNKDKTLVLQFSVRKHEQLDCGGYVKLLGGVDQKKFGGDTYSIMEGPDIC 143  
Qy 121 GPGTKKVVHVIENYKGNVLINKDIRCKDDETHLYTLIVRPDNTYEVKIDNSQVESGSL 179  
Db 144 GYSTKKVHTILT KDGNHLIRKDVPCETDQLTHVYTLIIRPDATYSILIDNEEKQTGSI 202

Search completed: January 9, 2002, 15:02:02  
Job time: 189 sec



GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: January 9, 2002, 15:12:15 ; Search time 25:18 Seconds  
(without alignments)  
50.964 Million cell updates/sec

Title: US-09-828-000-7  
Perfect score: 189  
Sequence: 1 VIFNYGKNVLINKIRCKDDEFTHLYTLIVRPDN 35

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 100059 seqs, 36664827 residues  
Total number of hits satisfying chosen parameters: 100059

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt\_39:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	189	100.0	416	1 CRTC_MOUSE	P14211 mus musculus
2	189	100.0	416	1 CRTC_RAT	P18418 rattus norv
3	189	100.0	416	1 CRTC_HUMAN	P27797 homo sapien
4	189	100.0	418	1 CRTC_RABIT	P15253 oryctolagus
5	184	97.4	400	1 CRT1_BOVIN	P52193 bos taurus
6	184	97.4	421	1 CRT2_BOVIN	P42918 bos taurus
7	158	83.6	406	1 CRTC_DROME	P29413 drosophila
8	139	73.5	388	1 RALL_ONCV	P11012 onchocerca
9	138	73.0	393	1 CRTC_SCHMA	Q06814 schistosoma
10	129	68.3	395	1 CRTC_CAEEL	P27798 caenorhabdi
11	126	66.7	420	1 CRTC_CHLRE	Q98td3 chlamydomon
12	110	58.2	416	1 CRTC_BETVU	O81919 beta vulgar
13	108.5	57.4	424	1 CRTC_DICDI	Q23858 dictyosteli
14	107	56.6	421	1 CRTC_PRUAR	Q9xf98 prunus arme
15	105	55.6	421	1 CRTC_RICCO	P93508 ricinus com
16	105	55.6	424	1 CRTC_ARATH	Q38858 arabidopsis
17	103	54.5	420	1 CRTC_MAIZE	Q9sp22 zea mays (m
18	102	54.0	424	1 CRTC_ARATH	O04153 arabidopsis
19	100	52.9	425	1 CRT1_ARATH	O04151 arabidopsis
20	98	51.9	424	1 CRTC_ORISA	Q9sly8 oryza sativ
21	94	49.7	416	1 CRTC_NICPL	Q04011 nicotiana p
22	90.5	47.9	416	1 CRTC_BERST	Q9zpp1 berberis st
23	90	47.6	401	1 CRTC_EUGGR	Q9znp3 euqlena gra
24	64	33.9	540	1 MTAL_ACICA	P25201 acinetobact
25	64	33.9	592	1 CALX_HUMAN	P27824 homo sapien
26	63	33.3	591	1 CALX_MOUSE	P35564 mus musculu
27	63	33.3	591	1 CALX_RAT	P35565 rattus norv
28	63	33.3	593	1 CALX_CANFA	P24643 canis fami
29	59	31.2	540	1 CALX_HELTU	Q39994 helianthus
30	58	30.7	546	1 CALX_SOYBN	Q39817 glycine max
31	55.5	29.4	611	1 CALG_MOUSE	P52194 mus musculu
32	54	28.6	530	1 CALX_ARATH	P29402 arabidopsis
33	54	28.6	610	1 CALG_HUMAN	O14967 homo sapien

34 54 28.6 619 1 CALX\_CAEEL  
35 51.5 27.2 463 1 VOHA\_CHICK  
36 51 27.0 725 1 NCA2\_MOUSE  
37 51 27.0 761 1 NCA2\_HUMAN  
38 51 27.0 848 1 NCA1\_HUMAN  
39 51 27.0 853 1 NCA1\_BOVIN  
40 51 27.0 858 1 NCA1\_RAT  
41 51 27.0 1091 1 NCA1\_CHICK  
42 51 27.0 1115 1 NCA1\_MOUSE  
43 50.5 26.7 236 1 VC05\_SPVKA  
44 50.5 26.7 560 1 CALX\_SCHPO  
45 50 26.5 1022 1 DP05\_YEAST

## ALIGNMENTS

RESULT 1  
CRTC\_MOUSE  
ID CRTC\_MOUSE STANDARD; PRT; 416 AA.  
AC P14211;  
DT 01-JAN-1990 (Rel. 13, Created)  
DT 01-JAN-1990 (Rel. 13, Last sequence update)  
DT 15-DEC-1998 (Rel. 37, Last annotation update)  
DE CALRETICULIN PRECURSOR (CRP55) (CALREGULIN) (HACBP) (ERP60).  
GN CALR.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A., AND SEQUENCE OF 18-48 AND 129-161.  
RX STRAIN=BALB/C; TISSUE=Liver;  
RX MEDLINE=90059955; PubMed=2583110;  
RA Smith M.J., Koch G.L.E.;  
RT "Multiple zones in the sequence of calreticulin (CRP55, calregulin, HACBP), a major calcium binding ER/SR protein.";  
RL EMBO J. 8:3581-3586(1989).  
RN [2]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=93013037; PubMed=1398135;  
RA Mazzarella R.A., Gold P., Cunningham M., Green M.;  
RT "Determination of the sequence of an expressible cDNA clone encoding ERp60/calregulin by the use of a novel nested set method.";  
RN [3]  
RP Gene 120:217-225(1992).  
RX SEQUENCE OF 18-38;  
RC TISSUE=Fibroblast;  
RX MEDLINE=95009907; PubMed=7523108;  
RA Merrick B.A., Patterson R.M., Wichter L.L., He C., Selkirk J.K.;  
RT "Separation and sequencing of familial and novel murine proteins using preparative two-dimensional gel electrophoresis.";  
RL Electrophoresis 15:735-745(1994).  
CC -!- FUNCTION: THIS PROTEIN BINDS CALCIUM. THERE ARE BOTH HIGH AND LOW AFFINITY CALCIUM-BINDING SITES.  
CC -!- SUBUNIT: MONOMER (BY SIMILARITY).  
CC -!- SUBCELLULAR LOCATION: ENDOPLASMIC RETICULUM LUMEN.  
CC -!- SIMILARITY: BELONGS TO THE CALRETICULIN FAMILY.  
CC -----  
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CC -----  
DR EMBL; X14926; CAA33053.1; -  
DR EMBL; M92988; AAA37569.1; -  
DR PIR; S06763; S06763.  
DR PIR; JCL1444; JCL1444.  
DR SWISS-2DPAGE; P14211; MOUSE.  
DR MGI; MGI:88252; Calr.

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DR InterPro; IPR001580; Calreticulin.
DR InterPro; IPR000886; ER_target.
DR Pfam; PF00262; calreticulin.1.
DR PRINTS; PR00626; CALRETICULIN.
DR PROSITE; PD001866; Calreticulin; 1.
DR PROSITE; PS00014; ER_TARGET; 1.
DR PROSITE; PS00803; CALRETICULIN_1; 1.
DR PROSITE; PS00804; CALRETICULIN_2; 1.
DR PROSITE; PS00805; CALRETICULIN_REPEAT; 3.
KW Endoplasmic reticulum; Calcium-binding; Repeat; Signal.
FT SIGNAL 1 17
FT CHAIN 18 416
FT DOMAIN 18 197
FT DOMAIN 18 197
FT DOMAIN 198 308
FT DOMAIN 309 416
FT DOMAIN 191 255
FT REPEAT 191 202
FT REPEAT 210 221
FT REPEAT 227 238
FT REPEAT 244 255
FT DOMAIN 259 297
FT REPEAT 259 289
FT REPEAT 273 283
FT REPEAT 287 297
FT DOMAIN 351 407
FT DISULFID 137 163
FT SITE 413 416
SQ SEQUENCE 416 AA; 47994 MW; 24C03B00913408D8 CRC64;

Query Match 100.0%; Score 189; DB 1; Length 416;
Best Local Similarity 100.0%; Pred. No. 3.4e-19;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VIFNYGKGVLYNKIDRCDDDETHLYTLIVRPDN 35
Db 146 VIFNYGKGVLYNKIDRCDDDETHLYTLIVRPDN 180

RESULT 2
CRTC_RAT
ID CRTC_RAT STANDARD; PRT; 416 AA.
AC P18418; P10452;
DT 01-MAR-1989 (Rel. 10, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE CALRETICULIN PRECURSOR (CRP55) (CALREGULIN) (HACBP) (ERP60) (CALBP)
DE (CALCIUM-BINDING PROTEIN 3) (CABP3).
GN CALR.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID 10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN SPRAGUE-DAWLEY; TISSUE Brain cortex;
RX MEDLINE 90370496; PubMed 2395661;
RA Murthy K.K., Banville D., Srikant C.B., Carrier F., Bell A.,
Holmes C., Patel Y.C.;
RT "Structural homology between the rat calreticulin gene product and
the Onchocerca volvulus antigen Ra1-1.";
RL Nucleic Acids Res. 18:4933-4933(1990).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN SPRAGUE-DAWLEY;
RX MEDLINE 93202172; PubMed 8453984;
RA Nakamura M., Moriya M., Baba T., Michikawa Y., Yamanobe T., Arai K.,
Okinaga S., Kobayashi T.;
RT "An endoplasmic reticulum protein, calreticulin, is transported into
the acrosome of rat sperm.";
RL Exp. Cell Res. 205:101-110(1993).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN SPRAGUE-DAWLEY; TISSUE Liver;
RX MEDLINE 95181573; PubMed-7876339;
RA Soenichsen B., Fuellekrug J., van Nguyen P., Diekmann W.,
Robinson D.G., Mieskes G.;
RT "Retention and retrieval: both mechanisms cooperate to maintain
calreticulin in the endoplasmic reticulum.";
RL J. Cell Sci. 107:2705-2717(1994).
RN [4]
RP SEQUENCE OF 270-358 FROM N.A.
RC STRAIN-SPRAGUE-DAWLEY;
RL Lone Y.C., Bailly A., Latruffe N.;
RL Submitted (DEC-1988) to the EMBL/GenBank/DBJ databases.
RN [5]
RP SEQUENCE OF 18-29.
RX MEDLINE-91054414; PubMed-2241926;
RA Treves S., de Mattei M., Lanfredi M., Villa A., Green N.M.,
MacLennan D.H., Meldolesi J., Pozzan T.;
RT "Calreticulin is a candidate for a calsequestrin-like function in
Ca2(+)-storage compartments (calciosomes) of liver and brain.";
RL Biochem. J. 271:473-480(1990).
RN [6]
RP SEQUENCE OF 18-32.
RC STRAIN SPRAGUE-DAWLEY; TISSUE Testis;
RX MEDLINE-92360010; PubMed-1497655;
RA Nakamura M., Michikawa Y., Baba T., Okinaga S., Arai K.;
RT "Calreticulin is present in the acrosome of spermatids of rat
testis.";
RL Biochem. Biophys. Res. Commun. 186:668-673(1992).
RN [7]
RP SEQUENCE OF 18-32.
RC STRAIN LEC; TISSUE Liver;
RX MEDLINE-94072621; PubMed-8251535;
RA Yokoi T., Nagayama S., Kajiwara R., Kawaguchi Y., Horiuchi R.,
Kamataki T.;
RT "Identification of protein disulfide isomerase and calreticulin as
autoimmune antigens in LEC strain of rats.";
RL Biochim. Biophys. Acta 1158:339-344(1993).
CC -!- FUNCTION: THIS PROTEIN BINDS CALCIUM. THERE ARE BOTH HIGH AND
LOW AFFINITY CALCIUM-BINDING SITES.
CC -!- SUBUNIT: MONOMER (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: ENDOPLASMIC RETICULUM LUMEN.
CC -!- SIMILARITY: BELONGS TO THE CALRETICULIN FAMILY.
CC -!- CAUTION: WAS ORIGINALLY (REF.2) THOUGHT TO BE D-BETA-
HYDROXYBUTYRATE DEHYDROGENASE.
CC -----
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CC -----
DR EMBL; D78308; BAA11345.1; -
DR EMBL; X53363; CAA37446.1; -
DR EMBL; X13702; CAA31987.1; ALT_SEQ.
DR EMBL; X79327; CAA55890.1; -
DR PIR; S04867; S04867.
DR PIR; S11205; S11205.
DR PIR; S13045; S13045.
DR PIR; A49176; A49176.
DR PIR; S45036; S45036.
DR PIR; JH0819; JH0819.
DR InterPro; IPR001580; Calreticulin.
DR InterPro; IPR000886; ER_target.
DR Pfam; PF00262; calreticulin.1.
DR PRINTS; PR00626; CALRETICULIN.
DR PROSITE; PD001866; Calreticulin; 1.
DR PROSITE; PS00014; ER_TARGET; 1.
DR PROSITE; PS00803; CALRETICULIN_1; 1.
DR PROSITE; PS00804; CALRETICULIN_2; 1.
DR PROSITE; PS00805; CALRETICULIN_REPEAT; 3.
KW Endoplasmic reticulum; Calcium-binding; Repeat; Signal.
KW

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DR PROSITE; PS00804; CALRETICULIN_2; 1.
DR PROSITE; PS00805; CALRETICULIN_REPEAT; 3.
KW Endoplasmic reticulum; Calcium-binding; Repeat; Signal.
FT SIGNAL 1 17
FT CHAIN 18 417 CALRETICULIN.
FT DOMAIN 18 197 N-DOMAIN.
FT DOMAIN 198 308 P-DOMAIN.
FT DOMAIN 309 417 C-DOMAIN.
FT DOMAIN 191 255 4 X APPROXIMATE REPEATS.
FT REPEAT 191 202 1-1.
FT REPEAT 210 221 1-2.
FT REPEAT 227 238 1-3.
FT REPEAT 244 255 1-4.
FT DOMAIN 259 297 3 X APPROXIMATE REPEATS.
FT REPEAT 259 269 2-1.
FT REPEAT 273 283 2-2.
FT REPEAT 287 297 2-3.
FT DOMAIN 351 408 ASP/GLU/LYS-RICH.
FT DISULFID 137 163 BY SIMILARITY.
FT SITE 414 417 PREVENT SECRETION FROM ER.
FT CONFLICT 35 35 MISSING (IN REF. 3).
SQ SEQUENCE 417 AA; 48141 MW; HC3/C3C0F1054FB2 CRC64;

Query Match 100.0%; Score 189; DB 1; Length 417;
Best Local Similarity 100.0%; Pred. No. 3.4e-19;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VIPNYGKNVLINKIRCKDDEFTHTLVIRPDN 35
DD 146 VIPNYGKNVLINKIRCKDDEFTHTLVIRPDN 180
|||||
QY 1 VIPNYGKNVLINKIRCKDDEFTHTLVIRPDN 35
DD 146 VIPNYGKNVLINKIRCKDDEFTHTLVIRPDN 180

RESULT 4
ID CRTC_RABIT STANDARD; PRT; 418 AA.
AC P15253;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE CALRETICULIN PRECURSOR (CRP55) (CALREGULIN) (HACBP) (ERP60).
GN CALR.
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID:9986;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-slow-twitch skeletal muscle;
RX MEDLINE 90094320; PubMed 2600080;
RA Fliegel L., Burns K., MacLennan D.H., Reithmeier R.A.F., Michalak M.;
RT "Molecular cloning of the high affinity calcium-binding protein
(calsequestrin) of skeletal muscle sarcoplasmic reticulum.";
RG J. Biol. Chem. 264:21522-21528(1989).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE Fast-twitch skeletal muscle;
RX MEDLINE 91282795; PubMed 2059224;
RA Fliegel L., Michalak M.;
RT "Fast-twitch and slow-twitch skeletal muscles express the same
isoform of calsequestrin.";
RL Biochem. Biophys. Res. Commun. 177:979-984(1991).
RN [3]
RP SEQUENCE OF 18-36.
RX MEDLINE 91054414; PubMed 2241926;
RA Treves S., de Mattei M., Lanfretti M., Villa A., Green N.M.,
RA MacLennan D.H., Meldolesi J., Pozzan T.;
RT "Calsequestrin is a candidate for a calsequestrin-like function in
Ca2(+)-storage compartments (calciosomes) of liver and brain.";
RL Biochem. J. 271:473-480(1990).
RN [4]
RP SEQUENCE OF 18-46.
RX MEDLINE 91201375; PubMed 2016321;

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RA Milner R.E., Baksh S., Shemanko C., Carpenter M.R., Smillie L.,
RA Vance J.E., Opas M., Michalak M.;
RT "Calsequestrin, and not calsequestrin, is the major calcium binding
protein of smooth muscle sarcoplasmic reticulum and liver endoplasmic
reticulum.";
RL J. Biol. Chem. 266:7155-7165(1991).
RN [5]
RP PARTIAL SEQUENCE.
RC TISSUE=Lung;
RX MEDLINE 92002038; PubMed 1911780;
RA Guan S., Falick A.M., Williams D.E., Cashman J.R.;
RT "Evidence for complex formation between rabbit lung flavin-containing
monooxygenase and calreticulin.";
RL Biochemistry 30:9892-9900(1991).
CC -!- FUNCTION: THIS PROTEIN BINDS CALCIUM. THERE ARE BOTH HIGH AND
CC -!- LOW AFFINITY CALCIUM-BINDING SITES.
CC -!- SUBUNIT: MONOMER (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: ENDOPLASMIC RETICULUM LUMEN.
CC -!- SIMILARITY: BELONGS TO THE CALRETICULIN FAMILY.
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CC -----
DR EMBL; J05138; AAA31188.1; -
DR PIR; A34154; A34154.
DR PIR; C33208; C33208.
DR PIR; D33208; D33208.
DR PIR; E33208; E33208.
DR PIR; F33208; F33208.
DR PIR; S13046; S13046.
DR PIR; S13047; S13047.
DR InterPro; IPR001580; Calreticulin.
DR InterPro; IPR000886; ER_target.
DR Pfam; PF00262; calreticulin; 1.
DR PRINTS; PR00626; CALRETICULIN.
DR ProDom; PD001866; Calreticulin; 1.
DR PROSITE; PS00014; ER_TARGET; 1.
DR PROSITE; PS00803; CALRETICULIN_1; 1.
DR PROSITE; PS00804; CALRETICULIN_2; 1.
DR PROSITE; PS00805; CALRETICULIN_REPEAT; 3.
KW Endoplasmic reticulum; Calcium-binding; Repeat; Signal.
FT SIGNAL 1 17
FT CHAIN 18 418 CALRETICULIN.
FT DOMAIN 18 197 N-DOMAIN.
FT DOMAIN 198 308 P-DOMAIN.
FT DOMAIN 309 418 C-DOMAIN.
FT DOMAIN 191 255 4 X APPROXIMATE REPEATS.
FT REPEAT 191 202 1-1.
FT REPEAT 210 221 1-2.
FT REPEAT 227 238 1-3.
FT REPEAT 244 255 1-4.
FT DOMAIN 259 297 3 X APPROXIMATE REPEATS.
FT REPEAT 259 269 2-1.
FT REPEAT 273 283 2-2.
FT REPEAT 287 297 2-3.
FT DOMAIN 351 408 ASP/GLU/LYS-RICH.
FT DISULFID 137 163 BY SIMILARITY.
FT SITE 415 418 PREVENT SECRETION FROM ER.
FT VARIANT 35 35 E -> D.
FT CONFLICT 90 90 P -> T (IN REF. 5).
SQ SEQUENCE 418 AA; 48275 MW; B6082B689DC763A6 CRC64;

Query Match 100.0%; Score 189; DB 1; Length 418;
Best Local Similarity 100.0%; Pred. No. 3.4e-19;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VIPNYGKNVLINKIRCKDDEFTHTLVIRPDN 35

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Db 146 VIFNYGKGNVLINKDIRCKDDEFTHTLVLRPN 180
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RESULT 5
CRTL_BOVIN
ID CRTL_BOVIN STANDARD: PRT: 400 AA.
AC P52193;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DE CALRETICULIN, BRAIN ISOFORM 1 (CRP55) (CALREGULIN) (HACBP).
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OX Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE.
RC TISSUE=Brain;
RX MEDLINE=94183174; PubMed=8135753;
RA Matsuoka K., Seta K., Yamakawa Y., Okuyama T., Shinoda T., Isobe T.;
RT "Covalent structure of bovine brain calreticulin.";
RL Biochem. J. 298:435-442(1994).
CC -!- FUNCTION: THIS PROTEIN BINDS CALCIUM. THERE ARE BOTH HIGH AND
CC LOW AFFINITY CALCIUM-BINDING SITES.
CC -!- SUBUNIT: MONOMER.
CC -!- SUBCELLULAR LOCATION: ENDOPLASMIC RETICULUM LUMEN.
CC -!- SIMILARITY: BELONGS TO THE CALRETICULIN FAMILY.
DR InterPro; IPR001580; Calreticulin.
DR Pfam; PF00262; calreticulin; 1.
DR ProDom; PD001866; Calreticulin; 1.
DR PROSITE; PS00014; ER_TARGET; 1.
DR PROSITE; PS00803; CALRETICULIN_1; 1.
DR PROSITE; PS00804; CALRETICULIN_2; 1.
DR PROSITE; PS00805; CALRETICULIN_REPEAT; 3.
KW Endoplasmic reticulum; Calcium-binding; Repeat; Glycoprotein.
FT DOMAIN 1 180
FT DOMAIN 181 291
FT DOMAIN 292 400
FT DOMAIN 401 400
FT REPEAT 174 238
FT REPEAT 174 238
FT REPEAT 174 238
FT REPEAT 193 204
FT REPEAT 210 221
FT REPEAT 227 238
FT REPEAT 242 280
FT REPEAT 242 252
FT REPEAT 256 266
FT REPEAT 270 280
FT REPEAT 280 280
FT DOMAIN 334 390
FT DOMAIN 390 390
FT DISULFID 120 146
FT CARBOHYD 162 162
FT SITE 397 400
SQ SEQUENCE 400 AA; 46381 MW; 7D4B68DFC689EEF1 CRC64;

Query Match 97.4%; Score 184; DB 1; Length 400;
Best Local Similarity 97.1%; Pred. No. 1.6e-18;
Matches 34; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VIFNYGKGNVLINKDIRCKDDEFTHTLVLRPN 35
|||||
Db 129 VIFNYGKGNVLINKDIRCKDDEFTHTLVLRPN 163
|||||
RESULT 6
CRTL_BOVIN
ID CRTL_BOVIN STANDARD: PRT: 421 AA.
AC P42918;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)

15-JUL-1998 (Rel. 36, Last annotation update)
DE CALRETICULIN, BRAIN ISOFORM 2 PRECURSOR (CRP55) (CALREGULIN) (HACBP).
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OX Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=93385184; PubMed=8373827;
RA Liu N., Fine R.E., Johnson R.J.;
RT "Comparison of cDNAs from bovine brain coding for two isoforms of
calreticulin.";
RL Biochim. Biophys. Acta 1202:70-76(1993).
CC -!- FUNCTION: THIS PROTEIN BINDS CALCIUM. THERE ARE BOTH HIGH AND
CC LOW AFFINITY CALCIUM-BINDING SITES.
CC -!- SUBUNIT: MONOMER (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: ENDOPLASMIC RETICULUM LUMEN.
CC -!- SIMILARITY: BELONGS TO THE CALRETICULIN FAMILY.
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CC -----
EMBL; L13462; AAC37307.1;
DR InterPro; IPR001580; Calreticulin.
DR Pfam; PF00262; calreticulin; 1.
DR PRINTS; PR00626; CALRETICULIN.
DR ProDom; PD001866; Calreticulin; 1.
DR PROSITE; PS00014; ER_TARGET; 1.
DR PROSITE; PS00803; CALRETICULIN_1; 1.
DR PROSITE; PS00804; CALRETICULIN_2; 1.
DR PROSITE; PS00805; CALRETICULIN_REPEAT; 3.
KW Endoplasmic reticulum; Calcium-binding; Repeat; Signal.
FT SIGNAL 1 34
FT CHAIN 35 421
FT DOMAIN 35 201
FT DOMAIN 202 312
FT DOMAIN 313 421
FT DOMAIN 195 259
FT REPEAT 195 206
FT REPEAT 214 225
FT REPEAT 231 242
FT REPEAT 248 259
FT DOMAIN 263 301
FT REPEAT 263 273
FT REPEAT 277 287
FT REPEAT 291 301
FT DOMAIN 366 411
FT DISULFID 141 167
FT CARBOHYD 183 183
FT SITE 418 421
SQ SEQUENCE 421 AA; 48812 MW; 0257E959F71528BC CRC64;

Query Match 97.4%; Score 184; DB 1; Length 421;
Best Local Similarity 97.1%; Pred. No. 1.7e-18;
Matches 34; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VIFNYGKGNVLINKDIRCKDDEFTHTLVLRPN 35
|||||
Db 150 VIFNYGKGNVLINKDIRCKDDEFTHTLVLRPN 184
|||||
RESULT 7
CRTL_DROME
ID CRTL_DROME STANDARD: PRT: 406 AA.
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FT REPEAT 246 257 1-4.
FT DOMAIN 260 298 3 X 11 AA APPROXIMATE REPEATS.
FT REPEAT 260 270 2-1.
FT REPEAT 274 284 2-2.
FT REPEAT 288 298 2-3.
FT DISULFID 105 137 BY SIMILARITY.
FT SITE 421 424 PREVENT SECRETION FROM ER (POTENTIAL).
SQ SEQUENCE 424 AA; 48350 MW; BAF273694F96FC37 CRC64;

Query Match 57.4%; Score 108.5; DB 1; Length 424;
Best Local Similarity 58.3%; Pred. No. 7.3e-08;
Matches 21; Conservative 6; Mismatches 8; Indels 1; Gaps 1;

QY 1 VFNKYGNVLLINKDI-RCKDDETHLYTLIVRPDN 35
   ||||| : : : : : || : : : : |||
DB 145 VILNYGKNHLIRKNEINKVETDQLTHQYTLVISPDN 180

RESULT 14
CRIC_PRUAR STANDARD; PRT; 421 AA.
AC Q9XF98;
DT 20-AUG-2001 (Rel. 40, Created)
DT 20-AUG-2001 (Rel. 40, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE CALRETICULIN PRECURSOR.
OS Prunus armeniaca (Apricot).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids I; Rosales; Rosaceae; Prunus.
OC NCBI_TaxID=36596;
RN [1]
RS SEQUENCE FROM N.A.
RC SPRAIN=CV, BERGERON; TISSUE=Mesocarp, and Endocarp;
RA Mbeugie-A-Mbeugie D., Fils-Lycaon B.R.;
RT "Molecular cloning and nucleotide sequence of a calreticulin from
RL apricot (Prunus armeniaca cv. Bergeron).";
RL Submitted (MAR-1995) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: THIS PROTEIN BINDS CALCIUM. THERE ARE BOTH HIGH AND
CC LOW AFFINITY CALCIUM-BINDING SITES (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: ENDOPLASMIC RETICULUM LUMEN (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE CALRETICULIN FAMILY.
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-----
CC EMBL: AF134733; AAD32207.1; -
DR InterPro: IPR001580; Calreticulin.
DR InterPro: IPR000886; ER_target.
DR Pfam: PF00262; calreticulin; 1.
DR PRINTS: PR00626; CALRETICULIN.
DR ProDom: PD001866; Calreticulin.
DR PROSITE: PS00014; ER_TARGET; 1.
DR PROSITE: PS00803; CALRETICULIN_1; 1.
DR PROSITE: PS00804; CALRETICULIN_2; 1.
DR PROSITE: PS00805; CALRETICULIN_REPEAT; 2.
DR Endoplasmic reticulum; Calcium-binding; Repeat; Signal; Glycoprotein.
FT SIGNAL 1 22 POTENTIAL.
FT CHAIN 23 421 CALRETICULIN.
FT CARBOHYD 56 56 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 156 156 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT SITE 418 421 PREVENT SECRETION FROM ER (POTENTIAL).
SQ SEQUENCE 421 AA; 48416 MW; 4F5F94CBAA6C6690 CRC64;

Query Match 56.6%; Score 107; DB 1; Length 421;
Best Local Similarity 54.5%; Pred. No. 1.2e-07;

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Matches 18; Conservative 5; Mismatches 10; Indels 0; Gaps 0;

Qy 2 IFNYKGNVLINKDIRCKDDEFTHLYTLIVRPD 34  
152 ILNYNTNLIKDKVPCETDQLTHVYTFIIRPD 184

## RESULT 15

CRIC_RICCO	ID	CRIC_RICCO	STANDARD;	PRT;	415 AA.
AC		P03508;			
DF		20-AUG-2001	(Rel. 40, Created)		
DF		20-AUG-2001	(Rel. 40, Last sequence update)		
DF		20-AUG-2001	(Rel. 40, Last annotation update)		
DE		CALRETTICULIN PRECURSOR.			
OS		Ricinus communis (Castor bean).			
OX		Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;			
OX		Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;			
OX		eurosid I; Malpighiales; Euphorbiaceae; Ricinus.			
OX		NCBI_TaxID 3988;			
RN		[1]			

RP SEQUENCE FROM N. A.

RX MEDLINE-97435975; Pubmed 9290642;  
 RA Coughlan S.J., Hastings C., Winfrey R. Jr.;  
 RT "Cloning and characterization of the calreticulin gene from Ricinus  
 RL communis L.;  
 RI Plant Mol. Biol. 34:897-911(1997).  
 CC -1- FUNCTION: THIS PROTEIN BINDS CALCIUM. THERE ARE BOTH HIGH AND  
 CC LOW AFFINITY CALCIUM-BINDING SITES.  
 CC -1- SUBCELLULAR LOCATION: ENDOPLASMIC RETICULUM LUMEN.  
 CC -1- SIMILARITY: BELONGS TO THE CALRETICULIN FAMILY.  
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DR	EMBL; U74631; AAB71420.1; -.
DR	EMBL; U74630; AAB71419.1; -.
DR	Mandel; 10452; Kico; i166; 10452.
DR	InterPro; IPR001580; Calreticulin.
DR	InterPro; IPR000886; ER_target.
DR	Pfam; PF00262; calreticulin; 1.
DR	PRINTS; PR00626; CALRETICULIN.
DR	PRODom; PD001866; Calreticulin; 1.
DR	PROSITE; PS00014; ER_TARGET; 1.
DR	PROSITE; PS00803; CALRETICULIN_1; 1.
DR	PROSITE; PS00804; CALRETICULIN_2; 1.
DR	PROSITE; PS00805; CALRETICULIN_REPEAT; 2.
KW	Endoplasmic reticulum; Calcium-binding; Repeat; Signal; Glycoprotein.
FT	SIGNAL 1 20 POTENTIAL.
FT	CHAIN 21 415 CALRETICULIN.
FT	CARBOHYD 52 52 N-LINKED (GLCNAC. .) (POTENTIAL).
FT	CARBOHYD 152 152 N-LINKED (GLCNAC. .) (POTENTIAL).
FT	SITE 412 415 PREVENT SECTECTION FROM ER.
SQ	SEQUENCE 415 AA; 47522 MW; DD5P452E76CC/F8C CRC64;

Query Match 55.6%; Score 105; DB 1; Length 415;  
Best Local Similarity 51.5%; Pred. NO. 2.2e-07;  
Matches 17; Conservative 7; Mismatches 9; Indels 0; Gaps 0;

```
Qy 2 IFNYKGNVLINKDIRCKDDDEFTHLYTLVIRPD 34
      | | | | | | | | | | | | | | | | | |
Db 148 ILNYDNTNHLIKKEVCEFTDQLTHVYTLVIRPD 180
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Search completed: January 9, 2002, 15:12:16  
Job time: 658 sec



GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: January 9, 2002, 15:03:29 ; Search time 78.15 Seconds  
(without alignments)  
65.509 Million cell updates/sec

Title: US-09-828-000-7  
Perfect score: 189  
Sequence: 1 VIFNYGKNVLINKRCKDDETHLYTLIVRPD 35

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 473505 seqs, 146272329 residues

Total number of hits satisfying chosen parameters: 473505

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL\_17:\*

- 1: sp\_archaea:\*
- 2: sp\_bacteria:\*
- 3: sp\_fungi:\*
- 4: sp\_human:\*
- 5: sp\_invertebrate:\*
- 6: sp\_mammal:\*
- 7: sp\_mhc:\*
- 8: sp\_organelle:\*
- 9: sp\_phase:\*
- 10: sp\_plant:\*
- 11: sp\_rodent:\*
- 12: sp\_virus:\*
- 13: sp\_vertebrate:\*
- 14: sp\_unclassified:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	173	91.5	318	13 Q9PTX7	Q9ptx7 lampetra re
2	169	89.4	421	5 Q9U6S0	Q9u6s0 strongyloce
3	168	88.9	405	5 Q26268	Q26268 aplysia cal
4	168	88.9	410	5 Q16893	Q16893 amblyomma a
5	161	85.2	343	13 Q91711	Q91711 xenopus lae
6	161	85.2	411	13 Q91710	Q91710 xenopus lae
7	158	83.6	406	5 Q9U916	Q9u916 drosophila
8	154	81.5	417	13 Q9PUC1	Q9pucl brachydanio
9	153	81.0	350	5 Q26514	Q26514 schistosoma
10	153	81.0	396	5 Q45034	Q45034 schistosoma
11	153	81.0	403	5 Q76961	Q76961 necator ame
12	148	78.3	419	13 Q98984	Q98984 rana rugosa
13	146	77.2	375	5 Q18478	Q18478 litomosoides
14	146	77.2	387	5 Q97372	Q97372 difofilaria
15	128	67.7	321	13 Q9U5G0	Q9u5g0 eptatretus
16	107	56.6	321	10 Q41799	Q41799 zea mays (m
17	107	56.6	421	10 Q43712	Q43712 zea mays (m
18	104	55.0	412	10 Q40040	Q40040 hordeum vul
19	104	55.0	415	10 Q40041	Q40041 hordeum vul

20	98.5	52.1	427	10 Q9FYV2	Q9fyv2 pinus taeda
21	98	51.9	422	10 Q22502	Q22502 brassica na
22	94	49.7	137	11 Q9D373	Q9d373 mus musculu
23	94	49.7	240	10 Q9ST29	Q9st29 solanum mel
24	94	49.7	380	11 Q9D906	Q9d906 mus musculu
25	94	49.7	389	10 Q40567	Q40567 nicotiana t
26	77	40.7	559	5 Q9NG26	Q9ng26 tritricomo
27	72	38.1	401	5 Q9U9N9	Q9u9n9 trypanosoma
28	72	38.1	403	5 Q9XYF8	Q9xyf8 trypanosoma
29	71	37.6	582	5 Q76214	Q76214 schistosoma
30	71	37.6	582	5 Q9TVF3	Q9tvf3 schistosoma
31	67.5	35.7	872	5 Q26045	Q26045 proliferati
32	66	34.9	397	5 Q94592	Q94592 leishmania
33	66	34.9	582	5 Q04702	Q04702 schistosoma
34	65	34.4	214	4 Q9UDG2	Q9udg2 homo sapien
35	64	33.9	540	2 Q53293	Q53293 acinetobact
36	64	33.9	541	2 Q56752	Q56752 bergeyella
37	63	33.3	291	5 Q9Y1V1	Q9y1v1 leishmania
38	61.5	32.5	455	5 Q9BMP7	Q9bmp7 plasmodium
39	60	31.7	581	5 Q9BLH3	Q9blh3 halocynthia
40	60	31.7	622	13 Q98985	Q98985 rana rugosa
41	59	31.2	543	5 Q9VVP4	Q9vvp4 drosophila
42	59	31.2	545	5 Q9VAL7	Q9val7 drosophila
43	59	31.2	556	5 Q917S9	Q917s9 drosophila
44	59	31.2	583	5 Q9VXF6	Q9vxf6 drosophila
45	59	31.2	605	5 Q02393	Q02393 drosophila

#### ALIGNMENTS

RESULT 1

Q9PTX7 PRELIMINARY; PRT; 318 AA.  
AC Q9PTX7:  
DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
DE 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)  
DE CALRETICULIN (FRAGMENT).  
OS Lampetra reissneri.  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Hyperoartia;  
OC Petromyzontiformes; Petromyzontidae; Lampetra.  
OX NCBI\_TaxID=7753;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=20063780; PubMed=10594174;  
RA Kuraku S., Hoshiyama D., Katoh K., Suga H., Miyata T.;  
RT "Monophyly of lampreys and hagfishes supported by nuclear DNA-coded  
genes.";  
RL J. Mol. Evol. 49:729-735(1999).  
DR EMBL: AB025328; BAA88481.1; -;  
DR InterPro: IPR000886; ER\_target.  
DR InterPro: IPR001580; Calreticulin.  
DR Pfam: PF00262; calreticulin; 1.  
DR PRINTS: PR00626; Calreticulin; 1.  
DR ProDom: PD001866; Calreticulin; 1.  
DR PROSITE: PS00804; CALRETICULIN\_2: 1.  
DR PROSITE: PS00805; CALRETICULIN\_REPEAT: 3.  
DR PROSITE: PS00014; ER\_TARGET; UNKNOWN\_1.  
DR NON\_TER 1  
SQ SEQUENCE 318 AA; 36997 MW; C88102EALCAC1506 CRC64;

Query Match 91.5%; Score 173; DB 13; Length 318;  
Best Local Similarity 94.1%; Pred. No. 3.4e-16;  
Matches 32; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 VIFNYGKNVLINKRCKDDETHLYTLIVRPD 34

||||||| ||||||| ||||||| ||||||| |||||||  
Db 45 VIFNYGKNVLINKRCKDDETHLYTLIVRPD 78

RESULT 2



Query Match	85.2%;	Score 161;	DB 13;	Length 411;
Best Local Similarity	85.7%;	Pred. No. 2.1e-14;		

RESULT	8
Q9PUC1	
ID	O9PUC1 PRELIMINARY; PRT; 417 AA.
AC	O9PUC1:
DT	01-MAY-2000 (TREMBlrel. 13, Created)
DT	01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT	01-JUN-2001 (TREMBlrel. 17, Last annotation update)
DE	CALRETICULIN.
OS	Brachydanio rerio (Zebrafish) (Zebra danio).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;
OC	Cypriniformes; Cyprinidae; Rasborinae; Danio.
OX	NCBI_TaxID=7955;
RN	[1]
RP	SEQUENCE FROM N.A.
RA	Rubinstein A.L.; Lee D.; Luo R.; Henion P.D.; Halpern M.E.;
RT	"Genes Dependent on Zebrafish cyclops Function Identified by AFLP
RT	Differential Gene Expression Screen.";
RL	Genes 0:0-0(1999).
DR	EMBL; AF195882; AAF13700.1; -;
DR	InterPro; IPR000886; ER_target.
DR	InterPro; IPR001580; Calreticulin.
DR	Pfam; PF00262; calreticulin; 1.

```
DR PRINTS; PR00626; CALRETICULIN.
DR PRODM; PD001866; Calreticulin; 1.
DR PROSITE; PS00803; CALRETICULIN_1; 1.
DR PROSITE; PS00804; CALRETICULIN_2; 1.
DR PROSITE; PS00805; CALRETICULIN_REPEAT; 3.
DR PROSITE; PS00014; ER_TARGET; UNKNOWN_1.
SQ SEQUENCE 417 AA; 48723 MW; 2000C5B4004699B6 CRC64;

Query Match      81.5%; Score 154; DB 13; Length 417;
Best Local Similarity 82.4%; Pred. No. 2e-13;
Matches 28; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 VIFNYKGNVLINKDIRCKDDEFTHTLYTLIVRPD 34
   |||||: || ||| ||||| |||||: |||
DB 146 VIFNYKGQNHLLIKKIDCKDDKDELTHLYTLILRPD 179

RESULT 9
ID Q26514 PRELIMINARY; PRT; 350 AA.
AC Q26514:
DT 01-NOV-1996 (TRENBLrel. 01, Created)
DT 01-NOV-1996 (TRENBLrel. 01, Last sequence update)
DT 01-JUN-2001 (TRENBLrel. 17, Last annotation update)
DE CALRETICULIN (FRAGMENT).
GN RAL-1.
OS Schistosoma japonicum (Blood fluke).
OC Eukaryota; Metazoa; Platyhelminthes; Neodermata;
OC Trematoda; Digenea; Strigeidida; Schistosomatoidea; Schistosomatidae;
OC Schistosoma.
OX NCBI_TaxID 6182;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN CHINESE;
RA Huggins M.C., Moloney N.A.;
RL Submitted (AUG-1993) to the EMBL/GenBank/DBJ databases.
DR EMBL; M80524; AAA29917.1; -.
DR InterPro; IPR000886; ER_target.
DR InterPro; IPR001580; Calreticulin.
DR Pfam; PF00626; Calreticulin; 1.
DR PRINTS; PR00626; CALRETICULIN.
DR PRODM; PD001866; Calreticulin; 1.
DR PROSITE; PS00803; CALRETICULIN_1; 1.
DR PROSITE; PS00804; CALRETICULIN_2; 1.
DR PROSITE; PS00805; CALRETICULIN_REPEAT; 1.
DR PROSITE; PS00014; ER_TARGET; UNKNOWN_1.
FT NON_TER 1
SQ SEQUENCE 350 AA; 40385 MW; 30FAB4E8BB685D1C CRC64;

Query Match      81.0%; Score 153; DB 5; Length 350;
Best Local Similarity 82.9%; Pred. No. 2.3e-13;
Matches 29; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 VIFNYKGNVLINKDIRCKDDEFTHTLYTLIVRPD 35
   |||||: || ||| ||||| |||||: |||
DB 99 VIFNYKGQNHLLIKKIDPKDDQKTHLYTLIVRPD 133

RESULT 10
ID O45034 PRELIMINARY; PRT; 396 AA.
AC O45034:
DT 01-JUN-1998 (TRENBLrel. 06, Created)
DT 01-JUN-1998 (TRENBLrel. 06, Last sequence update)
DT 01-JUN-2001 (TRENBLrel. 17, Last annotation update)
DE CALRETICULIN.
OS Schistosoma japonicum (Blood fluke).
OC Eukaryota; Metazoa; Platyhelminthes; Neodermata;
OC Trematoda; Digenea; Strigeidida; Schistosomatoidea; Schistosomatidae;
OC Schistosoma.
OX NCBI_TaxID 6182;
```

```
RN SEQUENCE FROM N.A.
RP STRAIN-PHILIPPINE (MINDORO);
RA Scott J.C.;
RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF044408; AAC0515.1; -.
DR InterPro; IPR000886; ER_target.
DR InterPro; IPR001580; Calreticulin.
DR Pfam; PF00262; calreticulin; 1.
DR PRINTS; PR00626; CALRETICULIN.
DR PRODM; PD001866; Calreticulin; 1.
DR PROSITE; PS00803; CALRETICULIN_1; 1.
DR PROSITE; PS00804; CALRETICULIN_2; 1.
DR PROSITE; PS00805; CALRETICULIN_REPEAT; 2.
DR PROSITE; PS00014; ER_TARGET; UNKNOWN_1.
SQ SEQUENCE 396 AA; 45813 MW; C57394C6FB4CD77B CRC64;

Query Match      81.0%; Score 153; DB 5; Length 396;
Best Local Similarity 82.9%; Pred. No. 2.6e-13;
Matches 29; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 VIFNYKGNVLINKDIRCKDDEFTHTLYTLIVRPD 35
   |||||: || ||| ||||| |||||: |||
DB 145 VIFNYKGQNHLLIKKIDPKDDQKTHLYTLIVRPD 179

RESULT 11
ID O76961 PRELIMINARY; PRT; 403 AA.
AC O76961:
DT 01-NOV-1998 (TRENBLrel. 08, Created)
DT 01-NOV-1998 (TRENBLrel. 08, Last sequence update)
DT 01-JUN-2001 (TRENBLrel. 17, Last annotation update)
DE CALRETICULIN PRECURSOR.
GN CRT.
OS Necator americanus.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabdilitida; Strongylida;
OC Ancylostomatoidae; Ancylostomatidae; Bunostominae; Necator.
OX NCBI_TaxID-51031;
RN [1]
RP SEQUENCE FROM N.A.
RA Pritchard D.I., Brown A., McElroy P., Loukas A., Girdwood K.,
RA Berry C., Fullkrug R., Beck E.;
RT "Calreticulin is a hookworm allergen.";
RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ006790; CAA07254.1; -.
DR InterPro; IPR000886; ER_target.
DR InterPro; IPR001580; Calreticulin.
DR Pfam; PF00262; calreticulin; 1.
DR PRINTS; PR00626; CALRETICULIN.
DR PRODM; PD001866; Calreticulin; 1.
DR PROSITE; PS00803; CALRETICULIN_1; 1.
DR PROSITE; PS00804; CALRETICULIN_2; 1.
DR PROSITE; PS00805; CALRETICULIN_REPEAT; 3.
DR PROSITE; PS00014; ER_TARGET; UNKNOWN_1.
KW Signal; Allergen.
FT SIGNAL 1 16 POTENTIAL.
SQ SEQUENCE 403 AA; 46833 MW; 21F38B0515487B6F CRC64;

Query Match      81.0%; Score 153; DB 5; Length 403;
Best Local Similarity 82.4%; Pred. No. 2.7e-13;
Matches 28; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 2 IFNYKGNVLINKDIRCKDDEFTHTLYTLIVRPD 35
   ||: ||||| || ||||| |||||: |||
DB 143 IFSYKGNHLLIKKIDCKDDKDELTHLYTLILNPD 176

RESULT 12
Q98984
ID Q98984 PRELIMINARY; PRT; 419 AA.
```

Q98984;  
 01-FEB-1997 (TREMBLrel. 02, Created)  
 01-FEB-1997 (TREMBLrel. 02, Last sequence update)  
 01-JUN-2001 (TREMBLrel. 17, Last annotation update)  
 DE CALRETICULIN.  
 OS Rana rugosa (Frog).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.  
 OX NCBI\_TaxID=84110;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=96234004; PubMed=8654561;  
 RA Yamamoto S., Nakamura M.: Cloning and expression in the liver of the  
 "Calnexin: its molecular cloning and expression in the liver of the  
 frog, Rana rugosa.";  
 RL FEBS Lett. 387:27-32(1996).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RA Yamamoto S.;  
 RT "Strong expression of the calreticulin gene in the liver of Rana  
 rugosa tadpoles.";  
 RL J. Exp. Zool. 0:0-0(1996).  
 DR EMBL: D78589; BAAL1425.1; -;  
 DR InterPro: IPR000886; ER\_target.  
 DR InterPro: IPR001580; Calreticulin.  
 DR Pfam: PF00262; calreticulin; 1.  
 DR PRINTS: PR00626; CALRETICULIN.  
 DR ProDom: PD001866; Calreticulin; 1.  
 DR PROSITE: PS00803; CALRETICULIN\_1; 1.  
 DR PROSITE: PS00804; CALRETICULIN\_2; 1.  
 DR PROSITE: PS00805; CALRETICULIN\_REPEAT; 3.  
 DR PROSITE: PS00014; ER\_TARGET; UNKNOWN\_1.  
 SQ SEQUENCE 419 AA; 48658 MW; 2C857036769673BF CRC64;

Query Match 78.3%; Score 148; DB 13; Length 419;  
 Best Local Similarity 80.0%; Pred. No. 1.4e-12;  
 Matches 28; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 VIFNYGKGNVLNKDIRCKDDETHLYTLIVRPN 35  
 DB 147 VIFNYGKGNVLNKDIRSKADYISHLYTLIVRPN 181  
 |||:||||:|||||:|:|||||:|||||

RESULT 13  
 018478 PRELIMINARY; PRT; 375 AA.  
 AC 018478;  
 DT 01-JAN-1998 (TREMBLrel. 05, Created)  
 DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)  
 DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)  
 DE RAL-1 PROTEIN (FRAGMENT).  
 OS Litomosoides sigmodontis.  
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Spirurida; Filarioidea;  
 OC Onchocercidae; Litomosoides.  
 OX NCBI\_TaxID=42156;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA MacLennan K., Hoffman W.H., Taylor D.W.;  
 RL Submitted (SEP-1997) to the EMBL/Genbank/DBJ databases.  
 DR EMBL: AJ001621; CAA04877.1; -;  
 DR InterPro: IPR001580; Calreticulin.  
 DR Pfam: PF00262; calreticulin; 1.  
 DR PRINTS: PR00626; CALRETICULIN.  
 DR ProDom: PD001866; Calreticulin; 1.  
 DR PROSITE: PS00803; CALRETICULIN\_1; 1.  
 DR PROSITE: PS00804; CALRETICULIN\_2; 1.  
 DR PROSITE: PS00805; CALRETICULIN\_REPEAT; 3.  
 FT NON\_TER 375 375  
 SQ SEQUENCE 375 AA; 43842 MW; 03F7642FBFF7A5B8 CRC64;

Query Match 77.2%; Score 146; DB 5; Length 375;

Best Local Similarity 77.1%; Pred. No. 2.4e-12;  
 Matches 27; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 1 VIFNYGKGNVLNKDIRCKDDETHLYTLIVRPN 35  
 DB 144 VIFHYKGRNHMKKDIRCKDDVETHLYTLIVNSDN 178  
 |||:||||:|:|||||:|||||:|

RESULT 14  
 097372 PRELIMINARY; PRT; 387 AA.  
 AC 097372;  
 DT 01-MAY-1999 (TREMBLrel. 10, Created)  
 DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)  
 DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)  
 DE CALRETICULIN PRECURSOR.  
 OS Dirofilaria immitis.  
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Spirurida; Filarioidea;  
 OC Onchocercidae; Dirofilaria.  
 OX NCBI\_TaxID=6287;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=99094497; PubMed=9879888;  
 RA Tsuji N., Morales T.H., Ozols V.V., Carmody A.B., Chandrashekar R.;  
 RT "Molecular characterization of a calcium-binding protein from the  
 filarial parasite Dirofilaria immitis.";  
 RL Mol. Biochem. Parasitol. 97:69-79(1998).  
 DR EMBL: AF052978; AAD03405.1; -;  
 DR InterPro: IPR001580; Calreticulin.  
 DR Pfam: PF00262; calreticulin; 1.  
 DR PRINTS: PR00626; CALRETICULIN.  
 DR ProDom: PD001866; Calreticulin; 1.  
 DR PROSITE: PS00803; CALRETICULIN\_1; 1.  
 DR PROSITE: PS00804; CALRETICULIN\_2; 1.  
 DR PROSITE: PS00805; CALRETICULIN\_REPEAT; 3.  
 KW Signal.  
 FT SIGNAL 1 18 POTENTIAL.  
 FT CHAIN 19 387 CALRETICULIN.  
 SQ SEQUENCE 387 AA; 44941 MW; E7741BF6AAFA5885 CRC64;

Query Match 77.2%; Score 146; DB 5; Length 387;  
 Best Local Similarity 77.1%; Pred. No. 2.4e-12;  
 Matches 27; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 1 VIFNYGKGNVLNKDIRCKDDETHLYTLIVRPN 35  
 DB 144 VIFHYKGRNHMKKDIRCKDDVETHLYTLIVNSDN 178  
 |||:||||:|:|||||:|||||:|

RESULT 15  
 0905G0 PRELIMINARY; PRT; 321 AA.  
 AC 0905G0;  
 DT 01-MAY-2000 (TREMBLrel. 13, Created)  
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)  
 DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)  
 DE CALRETICULIN (FRAGMENT).  
 OS Eptatretus burgeri (Inshore hagfish).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Hyperotreti; Myxiniiformes;  
 OC Myxiniidae; Eptatretinae; Eptatretus.  
 OX NCBI\_TaxID=7764;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=LIVER;  
 RX MEDLINE=20063780; PubMed=10594174;  
 RA Kuraku S., Hoshiyama D., Katoh K., Suga H., Miyata T.;  
 RT "Monophyly of lampreys and hagfishes supported by nuclear DNA-coded  
 genes.";  
 RL J. Mol. Evol. 49:729-735(1999).  
 DR EMBL: AB025323; BAA88476.1; -;  
 DR InterPro: IPR000886; ER\_target.  
 DR InterPro: IPR001580; Calreticulin.

DR Pfam; PF00262; calreticulin; 1.  
DR PRINTS; PR00626; CALRETICULIN.  
DR ProDom; PD001866; Calreticulin; 1.  
DR PROSITE; PS00804; CALRETICULIN\_2; 1.  
DR PROSITE; PS00805; CALRETICULIN\_REPEAT; 3.  
DR PROSITE; PS00014; ER\_TARGET; UNKNOWN\_1.  
FT NON\_TER 1  
SQ SEQUENCE 321 AA; 37367 MW; 6E8DFA98D42F7AEF CRC64;

Query Match 67.7%; Score 128; DB 13; Length 321;  
Best Local Similarity 67.6%; Pred. No. 6.4e-10;  
Matches 23; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

QY 1 VIFNYKKNVLLINKDIRCKDDETHLYTLIVRPD 34  
DB 45 VILNSGKNHLIKKVKCKDDETHLYTLMLYPD 78

Search completed: January 9, 2002, 15:03:30  
Job time: 272 sec

GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: January 9, 2002, 15:01:13 ; Search time 83.2 Seconds  
(without alignments)  
31.161 Million cell updates/sec

Title: US-09-828-000-7  
Perfect score: 189  
Sequence: 1 VIFNYGKNVINKDIRCKDDETHLYTLIVRPDN 35

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 522463 seqs, 74073290 residues

Total number of hits satisfying chosen parameters: 522463

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A\_Geneseq\_1101.\*

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1: /SID88/gcgdata/geneseq/geneseq/AA1980.DAT.*
2: /SID88/gcgdata/geneseq/geneseq/AA1981.DAT.*
3: /SID88/gcgdata/geneseq/geneseq/AA1982.DAT.*
4: /SID88/gcgdata/geneseq/geneseq/AA1983.DAT.*
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22: /SID88/gcgdata/geneseq/geneseq/AA2001.DAT.*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	189	100.0	60	21	Recombinant human
2	189	100.0	61	21	Recombinant human
3	189	100.0	180	21	Human vasostatin (
4	189	100.0	280	21	Recombinant delta-
5	189	100.0	400	21	Recombinant human
6	189	100.0	401	18	Calreticulin, Hom
7	189	100.0	417	10	60 kD Ro (Ro/SSA)
8	189	100.0	417	20	Calreticulin, Hom
9	189	100.0	417	21	Human MBP-calretic
10	175	92.6	49	21	Recombinant human
11	167	88.4	403	17	Flea calreticulin

12	139	73.5	336	12	AAR12312	Partial sequence o
13	107	56.6	122	20	AAV00924	Human cClqR bindin
14	107	56.6	122	20	AAV00926	Rat cClqR binding
15	105	55.6	415	22	AAB66341	Castor bean calret
16	105	55.6	415	22	AAB66343	Castor bean calret
17	99	52.4	122	20	AAV00925	Mouse cClqR bindin
18	98	51.9	385	21	AAB32385	Human secreted pro
19	97	51.3	312	21	AAG24609	Arabidopsis thalia
20	97	51.3	312	21	AAG47933	Arabidopsis thalia
21	97	51.3	332	21	AAV30998	Arabidopsis thalia
22	97	51.3	421	21	AAG24608	Arabidopsis thalia
23	97	51.3	421	21	AAG47932	Arabidopsis thalia
24	97	51.3	424	21	AAG24607	Arabidopsis thalia
25	97	51.3	424	21	AAG47931	Arabidopsis thalia
26	97	51.3	441	21	AAV30997	Arabidopsis thalia
27	97	51.3	444	21	AAV30996	Arabidopsis thalia
28	63	33.3	593	16	AAR71094	Calnexin sequence.
29	58.5	31.0	417	21	AAV77953	A. thaliana enviro
30	58	30.7	542	22	AAB66342	Castor bean calnex
31	54	28.6	394	21	AAG26285	Arabidopsis thalia
32	54	28.6	394	21	AAG45612	Arabidopsis thalia
33	54	28.6	530	21	AAG26284	Arabidopsis thalia
34	54	28.6	530	21	AAG45611	Arabidopsis thalia
35	54	28.6	567	21	AAG45610	Arabidopsis thalia
36	51	27.0	458	21	AAB40855	Human ORFX ORF619
37	51	27.0	848	21	AAV88565	Human NCAM 140kD i
38	50.5	26.7	236	18	AAW26427	Swinepox virus Hin
39	50.5	26.7	236	22	AAB68248	Protein encoded by
40	50	26.5	1188	21	AAB18183	Plasmodium falcipa
41	49	25.9	318	20	AAV28509	Fen(y205D) mutant
42	49	25.9	346	22	AAV93016	C glycosylated prote
43	48	25.4	17	20	AAV21879	Peptide Seq ID No:
44	48	25.4	17	20	AAV09101	Cell adhesion reco
45	48	25.4	17	21	AAV78215	N-CAM heparin bind

#### ALIGNMENTS

```

RESULT 1
ID AAY92354 standard; Protein; 60 AA.
XX
AC AAY92354;
DT
DT 10-AUG-2000 (first entry)
XX
DE Recombinant human calreticulin residues 121-180.
XX
KW MBP-calreticulin; maltose binding protein; angiogenesis; inhibition;
KW endothelial cell; anti-angiogenic; neuroprotective; antidiabetic;
KW cytostatic; dermalogical; immunosuppressive; antiinflammatory; hepatic;
KW anti-atherosclerotic; gastrointestinal; anti-arthritis; ophthalmic.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO2000020577-A1.
XX
PD 13-APR-2000.
XX
PF 05-OCT-1999; 99WO-US23240.
XX
PR 06-OCT-1998; 98US-0103438.
XX
PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX
PI Tosato G, Pike SE, Yao L;
XX
WPI; 2000-303767/26.
XX
PT Inhibiting endothelial cell growth and angiogenesis using calreticulin,
PT useful for suppressing tumor growth

```

XX PS Claim 4; Page 85; 99pp; English.

XX CC A novel method of inhibiting endothelial cell growth comprises

XX CC contacting the cells with calreticulin (or its fragments/variants).

XX CC Fragments of calreticulin causes at least 40% inhibition of angiogenesis,

XX CC tumor growth and/or endothelial cell growth (claimed). The method may be

XX CC used for inhibiting angiogenesis in a patient. The angiogenesis is

XX CC associated with a disease other than a tumor that is associated with

XX CC neovascularization (e.g. diabetic neuropathy, retrolental fibroplasia,

XX CC trachoma, neovascular glaucoma, psoriasis, angiofibromas, immune

XX CC inflammation, atherosclerosis, excessive wound repair, retinal

XX CC neovascularization, macular degeneration, corneal graft rejection,

XX CC contact lens overwear, Crohn's disease, non-immune inflammation,

XX CC rheumatoid arthritis, systemic lupus erythematosus, thyroiditis,

XX CC Goodpasture's syndrome, systemic vasculitis, scleroderma, Sjorgen's

XX CC syndrome, sarcoidosis and primary biliary cirrhosis). The method may

XX CC also be used for treating/inhibiting tumor growth especially

XX CC Kaposi's sarcoma (claimed).

SQ Sequence 60 AA;

Query Match 100.0%; Score 189; DB 21; Length 60;

Best Local Similarity 100.0%; Pred. No. 1.3e-22;

Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VFIFYGKKNVLINKDIRCKDDETHLYTLIVRPDN 35

Db 9 VFIFYGKKNVLINKDIRCKDDETHLYTLIVRPDN 43

RESULT 2

AAI92352

ID AAY92352 standard; Protein; 61 AA.

XX AC AAY92352;

XX DT 10-AUG-2000 (first entry)

XX DE Recombinant human calreticulin residues 120-180.

XX KW MBP-calreticulin; maltose binding protein; angiogenesis; inhibition;

XX KW endothelial cell; anti-angiogenic; neuroprotective; antidiabetic;

XX KW cytotatic; dermalogical; immunosuppressive; antiinflammatory; hepatic;

XX KW anti-atherosclerotic; gastrointestinal; anti-arthritis; ophthalmic.

XX OS Homo sapiens.

XX OS Synthetic.

XX PN WO200020577-A1.

XX PD 13-APR-2000.

XX PF 05-OCT-1999; 99WO-US23240.

XX PR 06-OCT-1998; 98US-0103438.

XX PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.

XX PI Tosato G, Pike SE, Yao L;

XX DR WPI; 2000-303767/26.

XX Inhibiting endothelial cell growth and angiogenesis using calreticulin,

XX useful for suppressing tumor growth

XX Claim 4; Page 82-83; 99pp; English.

XX A novel method of inhibiting endothelial cell growth comprises

XX contacting the cells with calreticulin (or its fragments/variants).

XX Fragments of calreticulin causes at least 40% inhibition of angiogenesis,

XX tumor growth and/or endothelial cell growth (claimed). The method may be

XX associated with a disease other than a tumor that is associated with

XX neovascularization (e.g. diabetic neuropathy, retrolental fibroplasia,

XX trachoma, neovascular glaucoma, psoriasis, angiofibromas, immune

XX inflammation, atherosclerosis, excessive wound repair, retinal

XX tumor growth and/or endothelial cell growth (claimed). The method may be

CC used for inhibiting angiogenesis in a patient. The angiogenesis is

CC associated with a disease other than a tumor that is associated with

CC neovascularization (e.g. diabetic neuropathy, retrolental fibroplasia,

CC trachoma, neovascular glaucoma, psoriasis, angiofibromas, immune

CC inflammation, atherosclerosis, excessive wound repair, retinal

CC neovascularization, macular degeneration, corneal graft rejection,

CC contact lens overwear, Crohn's disease, non-immune inflammation,

CC rheumatoid arthritis, systemic lupus erythematosus, thyroiditis,

CC Goodpasture's syndrome, systemic vasculitis, scleroderma, Sjorgen's

CC syndrome, sarcoidosis and primary biliary cirrhosis). The method may

CC also be used for treating/inhibiting tumor growth especially

CC Kaposi's sarcoma (claimed).

XX Sequence 61 AA;

Query Match 100.0%; Score 189; DB 21; Length 61;

Best Local Similarity 100.0%; Pred. No. 1.3e-22;

Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VFIFYGKKNVLINKDIRCKDDETHLYTLIVRPDN 35

Db 10 VFIFYGKKNVLINKDIRCKDDETHLYTLIVRPDN 44

RESULT 3

AAI92351

ID AAY92351 standard; Protein; 180 AA.

XX AC AAY92351;

XX DT 10-AUG-2000 (first entry)

XX DE Human vasostatin (calreticulin N-terminal 180 amino acids).

XX KW MBP-calreticulin; maltose binding protein; vasostatin; N-terminal;

XX KW angiogenesis; inhibition; endothelial cell; anti-angiogenic;

XX KW neuroprotective; antidiabetic; cytotatic; dermalogical; hepatic;

XX KW immunosuppressive; antiinflammatory; anti-atherosclerotic;

XX KW gastrointestinal; anti-arthritis; ophthalmic.

XX OS Homo sapiens.

XX OS Synthetic.

XX PN WO200020577-A1.

XX PD 13-APR-2000.

XX PF 05-OCT-1999; 99WO-US23240.

XX PR 06-OCT-1998; 98US-0103438.

XX PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.

XX PI Tosato G, Pike SE, Yao L;

XX DR WPI; 2000-303767/26.

XX Inhibiting endothelial cell growth and angiogenesis using calreticulin,

XX useful for suppressing tumor growth

XX Claim 4; Page 82; 99pp; English.

XX A novel method of inhibiting endothelial cell growth comprises

XX contacting the cells with calreticulin (or its fragments/variants).

XX Fragments of calreticulin causes at least 40% inhibition of angiogenesis,

XX tumor growth and/or endothelial cell growth (claimed). The method may be

XX used for inhibiting angiogenesis in a patient. The angiogenesis is

XX associated with a disease other than a tumor that is associated with

XX neovascularization (e.g. diabetic neuropathy, retrolental fibroplasia,

XX trachoma, neovascular glaucoma, psoriasis, angiofibromas, immune

XX inflammation, atherosclerosis, excessive wound repair, retinal

XX tumor growth and/or endothelial cell growth (claimed). The method may be



CC contact lens overwear, Crohn's disease, non-immune inflammation,  
 CC rheumatoid arthritis, systemic lupus erythematosus, thyroiditis,  
 CC Goodpasture's syndrome, systemic vasculitis, scleroderma, Sjorgen's  
 CC syndrome, sarcoidosis and primary biliary cirrhosis). The method may  
 CC also be used for treating/inhibiting tumor growth especially  
 CC Kaposi's sarcoma (claimed).  
 XX  
 SQ Sequence 180 AA;

Query Match 100.0%; Score 189; DB 21; Length 180;  
 Best Local Similarity 100.0%; Pred. No. 4.9e-22;  
 Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VIFNYGKNVLINKDIRCKDDETHLYTLIVRPDN 35  
 Db 129 vfnygknvlinkdirckddefthlytlivrpdn 163  
 |||||

RESULT 4  
 AAY92355  
 ID AAY92355 standard; Protein; 280 AA.  
 XX  
 AC AAY92355;  
 XX  
 DT 10-AUG-2000 (first entry)  
 XX  
 DE Recombinant delta-120 calreticulin.  
 XX  
 KW MBP-calreticulin; maltose binding protein; angiogenesis; inhibition;  
 KW endothelial cell; anti-angiogenic; neuroprotective; antidiabetic;  
 KW cytostatic; dermalogical; immunosuppressive; antiinflammatory; hepatic;  
 KW anti-atherosclerotic; gastrointestinal; anti-arthritis; ophthalmic.  
 XX  
 OS Homo sapiens.  
 OS Synthetic.  
 XX  
 PN WO200020577-A1.  
 XX  
 PD 13-APR-2000.  
 XX  
 PF 05-OCT-1999; 99WO-US23240.  
 XX  
 PR 06-OCT-1998; 98US-0103438.  
 XX  
 PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.  
 XX  
 PI Tosato G, Pike SE, Yao L;  
 XX  
 DR WPI; 2000-303767/26.  
 XX  
 PT Inhibiting endothelial cell growth and angiogenesis using calreticulin,  
 PT useful for suppressing tumor growth  
 XX  
 PS Claim 4; Page 86; 99pp; English.  
 XX  
 CC This sequence comprises recombinant human calreticulin (AAY92350)  
 CC missing the N-terminal 120 amino acids.  
 CC A novel method of inhibiting endothelial cell growth comprises  
 CC contacting the cells with calreticulin (or its fragments/variants).  
 CC Fragments of calreticulin causes at least 40% inhibition of  
 CC angiogenesis, tumor growth and/or endothelial cell growth (claimed). The  
 CC method may be used for inhibiting angiogenesis in a patient. The  
 CC angiogenesis is associated with a disease other than a tumor that is  
 CC associated with neovascularization (e.g. diabetic neuropathy, retrolental  
 CC fibroplasia, trachoma, neovascular glaucoma, psoriasis, angiofibromas,  
 CC immune inflammation, atherosclerosis, excessive wound repair, retinal  
 CC neovascularization, macular degeneration, corneal graft rejection,  
 CC contact lens overwear, Crohn's disease, non-immune inflammation,  
 CC rheumatoid arthritis, systemic lupus erythematosus, thyroiditis,  
 CC Goodpasture's syndrome, systemic vasculitis, scleroderma, Sjorgen's  
 CC syndrome, sarcoidosis and primary biliary cirrhosis). The method may  
 CC also be used for treating/inhibiting tumor growth especially

CC Kaposi's sarcoma (claimed).  
 XX  
 SQ Sequence 280 AA;

Query Match 100.0%; Score 189; DB 21; Length 280;  
 Best Local Similarity 100.0%; Pred. No. 8.4e-22;  
 Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VIFNYGKNVLINKDIRCKDDETHLYTLIVRPDN 35  
 Db 9 vfnygknvlinkdirckddefthlytlivrpdn 43  
 |||||

RESULT 5  
 AAY92350  
 ID AAY92350 standard; Protein; 400 AA.  
 XX  
 AC AAY92350;  
 XX  
 DT 10-AUG-2000 (first entry)  
 XX  
 DE Recombinant human MBP-calreticulin.  
 XX  
 KW MBP-calreticulin; maltose binding protein; angiogenesis; inhibition;  
 KW endothelial cell; anti-angiogenic; neuroprotective; antidiabetic;  
 KW cytostatic; dermalogical; immunosuppressive; antiinflammatory; hepatic;  
 KW anti-atherosclerotic; gastrointestinal; anti-arthritis; ophthalmic.  
 XX  
 OS Homo sapiens.  
 OS WO200020577-A1.  
 XX  
 PD 13-APR-2000.  
 XX  
 PF 05-OCT-1999; 99WO-US23240.  
 XX  
 PR 06-OCT-1998; 98US-0103438.  
 XX  
 PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.  
 XX  
 PI Tosato G, Pike SE, Yao L;  
 XX  
 DR WPI; 2000-303767/26.  
 XX  
 PR N-PSDB; AAA09346, AAA09347.  
 XX  
 PT Inhibiting endothelial cell growth and angiogenesis using calreticulin,  
 PT useful for suppressing tumor growth  
 XX  
 PS Claim 4; Page 80-81; 99pp; English.  
 XX  
 CC Recombinant human MBP-calreticulin comprises the sequence of human  
 CC calreticulin (see AAY92349) without the 17 N-terminal amino acids.  
 CC A novel method of inhibiting endothelial cell growth comprises  
 CC contacting the cells with calreticulin (or its fragments/variants).  
 CC Fragments of calreticulin causes at least 40% inhibition of  
 CC angiogenesis, tumor growth and/or endothelial cell growth (claimed). The  
 CC method may be used for inhibiting angiogenesis in a patient. The  
 CC angiogenesis is associated with a disease other than a tumor that is  
 CC associated with neovascularization (e.g. diabetic neuropathy, retrolental  
 CC fibroplasia, trachoma, neovascular glaucoma, psoriasis, angiofibromas,  
 CC immune inflammation, atherosclerosis, excessive wound repair, retinal  
 CC neovascularization, macular degeneration, corneal graft rejection,  
 CC contact lens overwear, Crohn's disease, non-immune inflammation,  
 CC rheumatoid arthritis, systemic lupus erythematosus, thyroiditis,  
 CC Goodpasture's syndrome, systemic vasculitis, scleroderma, Sjorgen's  
 CC syndrome, sarcoidosis and primary biliary cirrhosis). The method may  
 CC also be used for treating/inhibiting tumor growth especially  
 CC Kaposi's sarcoma (claimed).  
 XX  
 SQ Sequence 400 AA;

Query Match 100.0%; Score 189; DB 21; Length 400;  
 Best Local Similarity 100.0%; Pred. No. 1.3e-21;  
 Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VIFNYGKNVINKIRCKDDETHLYTLIVRPDN 35  
 |||  
 Db 129 vifnygknvlnkirkckddefthlytlivrpdn 163

## RESULT 6

AAW11156  
 ID AAW11156 standard; peptide; 401 AA.

XX  
 AC AAW11156;

DT 31-MAY-1997 (first entry)

XX Calreticulin.

XX calreticulin; C-domain; restenosis; inhibitor.

XX Homo sapiens.

XX WO9636643-A1.

XX 21-NOV-1996.

XX 17-MAY-1996; 96WO-IB00471.

XX 16-MAY-1996; 96US-0649417.

XX 17-MAY-1995; 95US-0442844.

XX (UYAL-) UNIV ALBERTA.

XX Lucas A, Michalak M;

XX WPI; 1997-012036/01.

XX Inhibition of restenosis in patients - using calreticulin or a  
 PT C-domain polypeptide of calreticulin or a variant with the same  
 PT activity.

XX Disclosure; Fig 1; 48pp; English.

XX The present sequence is calreticulin. It and a C-domain derived peptide  
 CC (AAW06736) are useful for treating a patient to inhibit restenosis. The  
 CC calreticulin-type cpds. are administered either parenterally,  
 CC intravenously or via a catheter and can target areas of vascular damage  
 CC to inhibit or prevent restenosis.

XX Sequence 401 AA;

Query Match 100.0%; Score 189; DB 18; Length 401;  
 Best Local Similarity 100.0%; Pred. No. 1.3e-21;  
 Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VIFNYGKNVINKIRCKDDETHLYTLIVRPDN 35  
 |||  
 Db 129 vifnygknvlnkirkckddefthlytlivrpdn 163

## RESULT 7

AAW92276

ID AAP92276 standard; protein; 417 AA.

XX  
 AC AAP92276;

DT 23-FEB-1990 (first entry)

XX 60 kD Ro (Ro/SSA) antigen.

XX Sjogren's syndrome; systemic lupus erythematosus.

XX Synthetic.  
 OS WO8909273-A.  
 PN  
 XX  
 PD 05-OCT-1989.  
 XX  
 XX 22-MAR-1989; 89WO-US01213.  
 XX  
 PR 22-MAR-1988; 88US-0171634.  
 XX  
 XX (TEXA ) UNIV OF TEXAS SYST.  
 XX Sontheimer RD, Capra JD, McCauliffe DP;  
 PI  
 XX WPI; 1989-309537/42.  
 DR N-PSDB; AAP92276.  
 XX  
 XX DNA sequences encoding antigenic epitope(s) of Ro 60 kD autoantigen  
 PT - used in immunoassays to detect rheumatic disease  
 XX  
 XX Disclosure; Fig 2; 88pp; English.  
 XX  
 CC Synthetic peptides corresp. to an epitopic core of Ro antigen are  
 CC expressed recombinantly to detect autoantibodies, for identification  
 CC of autoimmune diseases. These epitopes are AAS 24-36, 23-36, 188-209,  
 CC or 241-255. The peptides may be substd. for ribonucleoprotein particle  
 CC antigens.  
 XX  
 XX Sequence 417 AA;

Query Match 100.0%; Score 189; DB 10; Length 417;  
 Best Local Similarity 100.0%; Pred. No. 1.4e-21;  
 Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VIFNYGKNVINKIRCKDDETHLYTLIVRPDN 35  
 |||  
 Db 146 vifnygknvlnkirkckddefthlytlivrpdn 180

## RESULT 8

AAW00927

ID AAY00927 standard; Protein; 417 AA.

XX  
 AC AAY00927;

XX 28-MAY-1999 (first entry)

XX Calreticulin.

XX Clq and collectin receptor; cClqR binding domain; complement ublquitin;  
 KW CUB functionality; inhibitor; complement activation; inflammation;  
 KW myocardial infarction; brain ischaemia; gut ischaemia; amyloid plaque;  
 KW rheumatoid arthritis; systemic lupus erythematosus; Alzheimer's disease;  
 KW immune complex nephritis; therapy.

XX Homo sapiens.

XX WO9907406-A1.

XX 18-FEB-1999.

XX 12-AUG-1998; 98WO-GB02430.

XX 12-AUG-1997; 97GB-0016998.

XX (UYLE-) UNIV LEICESTER.

XX Schwaebler W;

XX WPI; 1999-180404/15.

XX

PS Disclosure; Page 79-80; 99pp; English.

CC contacting the cells with calcitriol (or its analogues/variants).  
CC Fragments of calcitriol causes at least 40% inhibition of angiogenesis,  
CC tumor growth and/or endothelial cell growth (claimed). The method may be  
CC used for inhibiting angiogenesis in a patient. The angiogenesis is  
CC associated with a disease other than a tumor that is associated with

Sequence 403 AA;

The sequence was deduced from a cDNA clone lambda RAL-1 prep'd. from RNA isolated from nodules excised from patients infected with *O. volutus*. The N-terminal is incomplete, however Abs which specifically bind to protein prep'd. from induced cultures of lambda RAL-1 lysogens recognise a single polypeptide of mol. wt. 42,000 in extracts of adult worms. Analysis deduced sequence suggests that it encodes a protein of mol. wt. 39,130. If the antigen is not subject to post-translational processing this suggests that most of the coding sequence is present. The three repeats are highly hydrophilic regions likely to be exposed on the surface of the antigen and highly immunogenic. Recombinant antigen expressed by the clone can be used to stimulate T-cells of individuals infected by the parasite to proliferate and may be used as the basis for a vaccine against Onchocerciasis or river blindness.

SQ Sequence 336 AA;

Query Match 73.5%; Score 139; DB 12; Length 336;  
Best Local Similarity 74.3%; Pred. No. 9.2e-14;  
Matches 26; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY 1 VIFNYKGNVLINKDIRCKDDFTHTLYTLIVRPDN 35  
||||| : | ||||| ||||| ||  
Db 92 vifhykdnhmikkdirckddvfthtlytlivnsdn 126

## RESULT 13

AAAY00924  
ID AAY00924 standard; Protein; 122 AA.

XX AC AAY00924;

XX DT 28-MAY-1999 (first entry)

XX DE Human cClqR binding domain protein sequence.

XX KW Clq and collectin receptor; cClqR binding domain; complement ubiquitin;  
XX KW CUB functionality; inhibitor; complement activation; inflammation;  
XX KW myocardial infarction; brain ischaemia; gut ischaemia; amyloid plaque;  
XX KW rheumatoid arthritis; systemic lupus erythematosus; Alzheimer's disease;  
XX KW immune complex nephritis; therapy.

XX OS Homo sapiens.

XX PA WO9907406-A1.

XX PD 18-FEB-1999.

XX PF 12-AUG-1998; 98WO-GB02430.

XX PR 12-AUG-1997; 97GB-0016998.

XX PS (UYLE-) UNIV LEICESTER.

XX PI Schwaeble W;

XX WPI; 1999-180404/15.

XX DR N-PSDB; AAX27251.

XX PT Use of a cClqR binding domain - to modulate complement ubiquitin  
XX PT (CUB) functionality.

XX PS Claim 9; Page 23; 31pp; English.

XX CC This sequence is a Clq and collectin receptor (cClqR) binding  
XX CC domain. The invention relates to the use of a cClqR binding domain in a  
XX CC medicament to effect complement ubiquitin (CUB) functionality, and an  
XX CC inhibitor of the cClqR binding domain in a medicament to inhibit CUB  
XX CC functionality. The cClqR binding domain, or its inhibitor, can be used to  
XX CC treat a human or animal body. Particularly an inhibitor is used to treat  
XX CC complement activation involved in the initiation and maintenance of  
XX CC inflammation, for example in myocardial infarction, brain ischaemia  
XX CC (stroke), gut ischaemia, rheumatoid arthritis, systemic lupus  
XX CC erythematosus, burns, immune complex nephritis, and to treat amyloid  
XX CC plaques in Alzheimer's disease. The use of cClqR binding domain or  
XX CC inhibitor enables the CUB domain functionality to be modulated using a  
XX CC low molecular weight molecule.

SQ Sequence 122 AA;

Query Match 56.6%; Score 107; DB 20; Length 122;  
Best Local Similarity 100.0%; Pred. No. 3.2e-09;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 17 RCKDDEFTHLYTLIVRPDN 35  
||||| ||||| ||||| |||||

Db 1 rckddefthlytlivrpdn 19

## RESULT 14

AAAY00926  
ID AAY00926 standard; Protein; 122 AA.

XX AC AAY00926;

XX DT 28-MAY-1999 (first entry)

XX DE Rat cClqR binding domain protein sequence.

XX KW Clq and collectin receptor; cClqR binding domain; complement ubiquitin;  
XX KW CUB functionality; inhibitor; complement activation; inflammation;  
XX KW myocardial infarction; brain ischaemia; gut ischaemia; amyloid plaque;  
XX KW rheumatoid arthritis; systemic lupus erythematosus; Alzheimer's disease;  
XX KW immune complex nephritis; therapy.

XX OS Rattus norvegicus.

XX PN WO9907406-A1.

XX PD 18-FEB-1999.

XX PF 12-AUG-1998; 98WO-GB02430.

XX PR 12-AUG-1997; 97GB-0016998.

XX PA (UYLE-) UNIV LEICESTER.

XX PI Schwaeble W;

XX WPI; 1999-180404/15.

XX DR N-PSDB; AAX27253.

XX PT Use of a cClqR binding domain - to modulate complement ubiquitin  
XX PT (CUB) functionality.

XX PS Claim 9; Page 24-25; 31pp; English.

XX CC This sequence is a Clq and collectin receptor (cClqR) binding  
XX CC domain. The invention relates to the use of a cClqR binding domain in a  
XX CC medicament to effect complement ubiquitin (CUB) functionality, and an  
XX CC inhibitor of the cClqR binding domain in a medicament to inhibit CUB  
XX CC functionality. The cClqR binding domain, or its inhibitor, can be used to  
XX CC treat a human or animal body. Particularly an inhibitor is used to treat  
XX CC complement activation involved in the initiation and maintenance of  
XX CC inflammation, for example in myocardial infarction, brain ischaemia  
XX CC (stroke), gut ischaemia, rheumatoid arthritis, systemic lupus  
XX CC erythematosus, burns, immune complex nephritis, and to treat amyloid  
XX CC plaques in Alzheimer's disease. The use of cClqR binding domain or  
XX CC inhibitor enables the CUB domain functionality to be modulated using a  
XX CC low molecular weight molecule.

SQ Sequence 122 AA;

Query Match 56.6%; Score 107; DB 20; Length 122;  
Best Local Similarity 100.0%; Pred. No. 3.2e-09;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 17 RCKDDEFTHLYTLIVRPDN 35  
||||| ||||| ||||| |||||

## RESULT 15

AAB66341  
ID AAB66341 standard; Protein; 415 AA.

XX AC AAB66341;

DT 05-APR-2001 (first entry)  
XX  
DE Castor bean calreticulin SEQ ID NO: 2.  
XX  
KW Castor bean; calreticulin; calcium binding; er; endoplasmic reticulum;  
XX calnexin; promoter; resistance.  
XX  
OS Ricinus communis.  
XX  
PN US6171864-B1.  
XX  
PD 09-JAN-2001.  
XX  
PF 05-JUL-1996; 96US-0675816.  
XX  
PR 05-JUL-1996; 96US-0675816.  
XX  
PA (PION-) PIONEER HI-BRED INT INC.  
XX  
PI Coughlan SJ, Winfrey RJ;  
XX  
DI WPI: 2001-122335/13.  
DR N-PSDB; AAF29741, AAF29742.  
XX  
PT New nucleic acid molecules encoding a calcium binding chaperone protein  
PT in endoplasmic reticulum, calreticulin, and calreticulin promoter  
PT sequences, useful for producing foreign gene products in plant cells -  
XX  
PS Claim 1; Fig 3; 45pp; English.  
XX  
CC The present invention provides the protein and coding sequences for the  
CC castor bean calreticulin protein and the calreticulin promoter sequence.  
CC In addition, the castor bean calnexin protein, coding sequence and  
CC promoter are also described. Calreticulin and calnexin are calcium  
CC binding proteins found in the endoplasmic reticulum (er). The  
CC calreticulin promoter sequence can be used in vectors to promote the  
CC expression of foreign genes, particularly resistance genes, in plant  
CC cells.  
XX  
SQ Sequence 415 AA;  
  
Query Match 55.6%; Score 105; DB 22; Length 415;  
Best Local Similarity 51.5%; Pred. No. 3e-08;  
Matches 17; Conservative 7; Mismatches 9; Indels 0; Gaps 0;  
  
QY 2 IFNYKKNVLIINKDIRCKDDEFTHLTYTLIVRPD 34  
| | | | | : : : : :  
DB 148 IINYDTHLHKKEVPCETDQITHVYTLVIRPD 180  
  
Search completed: January 9, 2002, 15:01:14  
Job time: 160 sec

GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: January 9, 2002, 15:03:28 ; Search time 78.15 Seconds  
(without alignments)  
33.690 Million cell updates/sec

Title: US-09-828-000-6  
Perfect score: 96  
Sequence: 1 VIFNYKGNVLINKDIRC 18

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 473505 seqs, 146272329 residues

Total number of hits satisfying chosen parameters: 473505

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL\_17:\*  
1: sp-archaea:\*  
2: sp-bacteria:\*  
3: sp-fungi:\*  
4: sp-human:\*  
5: sp-invertebrate:\*  
6: sp-mammal:\*  
7: sp-mhc:\*  
8: sp-organelle:\*  
9: sp-phage:\*  
10: sp-plant:\*  
11: sp-rodent:\*  
12: sp-virus:\*  
13: sp-vertebrate:\*  
14: sp-unclassified:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	89	92.7	318	13 Q9PTX7	Q9ptx7 lampetra re
2	87	90.6	421	5 Q9U6S0	Q9u6s0 strongyloce
3	86	89.6	405	5 Q26268	Q26268 aplysia cal
4	85	88.5	410	5 Q16893	Q16893 amblyomma a
5	79	82.3	406	5 Q9U916	Q9u916 drosophila
6	78	81.2	419	13 Q98984	Q98984 rana rugosa
7	76	79.2	417	13 Q9PUC1	Q9puc1 brachydanio
8	74	77.1	403	5 Q76961	Q76961 necator ame
9	73	76.0	343	13 Q91711	Q91711 xenopus lae
10	73	76.0	375	5 Q18478	Q18478 litomosoid
11	73	76.0	387	5 Q97372	Q97372 dirofilaria
12	73	76.0	411	13 Q91710	Q91710 xenopus lae
13	72	75.0	350	5 Q26514	Q26514 schistosoma
14	72	75.0	396	5 Q45034	Q45034 schistosoma
15	60	62.5	321	13 Q9U5G0	Q9u5g0 eptatretus
16	51	53.1	348	4 Q00557	Q00557 homo sapien
17	49	51.0	506	13 Q73736	Q73736 brachydanio
18	49	51.0	506	13 Q9DGI6	Q9dgi6 brachydanio
19	48	50.0	247	2 Q48830	Q48830 lactobacill

20	48	50.0	846	13	057577	057577 cynops pyrr
21	48	50.0	1100	13	057576	057576 cynops pyrr
22	47	49.0	725	13	073633	073633 xenopus lae
23	47	49.0	725	13	073634	073634 xenopus lae
24	46	47.9	576	10	Q9LUV5	Q9luy5 arabidopsis
25	45	46.9	412	10	Q40040	Q40040 hordeum vul
26	45	46.9	415	10	Q40041	Q40041 hordeum vul
27	45	46.9	501	1	057693	057693 thermoprote
28	44.5	46.4	339	10	Q9AW69	Q9aw69 guillardia
29	44.5	46.4	781	12	Q82857	Q82857 jembrana di
30	44	45.8	321	10	Q41799	Q41799 zea mays (m
31	44	45.8	421	10	Q43712	Q43712 zea mays (m
32	44	45.8	631	12	Q9DHM5	Q9dhm5 yaba-like d
33	43	44.8	103	1	058084	058084 pyrococcus
34	43	44.8	250	6	P79232	P79232 papio hamad
35	43	44.8	257	1	Q9UZY6	Q9uzy6 pyrococcus
36	43	44.8	270	2	Q44795	Q44795 borrelia bu
37	43	44.8	270	2	Q9L9N5	Q9l9n5 borrelia bu
38	43	44.8	318	10	Q40126	Q40126 lycopersico
39	43	44.8	372	8	Q9XPX5	Q9xpx5 spyrldium p
40	43	44.8	372	8	Q9XPX3	Q9xpx3 adolphia ca
41	43	44.8	395	8	Q9TNG4	Q9tng4 datisca can
42	43	44.8	502	12	Q9ICT8	Q9ict8 chimpanzee
43	43	44.8	528	5	Q9UAF9	Q9uaf9 ephydatia f
44	43	44.8	654	10	Q9SGI7	Q9sg17 arabidopsis
45	43	44.8	743	10	Q9MAS2	Q9mas2 arabidopsis

#### ALIGNMENTS

RESULT 1  
Q9PTX7  
ID Q9PTX7 PRELIMINARY; PRT; 318 AA.  
AC Q9PTX7;  
DT 01-MAY-2000 (TRENBLrel. 13, Created)  
DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)  
DT 01-JUN-2001 (TRENBLrel. 17, Last annotation update)  
DE CALRETICULIN (FRAGMENT).  
OS Lampetra reissneri.  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Hyperoartia;  
OC Petromyzontiformes; Petromyzontidae; Lampetra.  
OX NCBI\_TaxID=7753;  
RN [1]

RP SEQUENCE FROM N.A.  
RX MEDLINE=20063780; PubMed=10594174;  
RA Kuraku S., Hoshiyama D., Katoh K., Suga H., Miyata T.;  
RT "Monophyly of lampreys and hagfishes supported by nuclear DNA-coded  
genes.";  
RL J. Mol. Evol. 49:729-735(1999).  
DR EMBL; AB025328; BAA88481.1; .  
DR InterPro; IPR000886; ER target.  
DR InterPro; IPR001580; Calreticulin.  
DR Pfam; PF00262; calreticulin; 1.  
DR PRINTS; PRO0626; CALRETICULIN.  
DR ProDom; PD001866; Calreticulin; 1.  
DR PROSITE; PS00804; CALRETICULIN\_2; 1.  
DR PROSITE; PS00805; CALRETICULIN\_REPEAT; 3.  
DR PROSITE; PS00014; ER\_TARGET; UNKNOWN\_1.  
FT NON\_TER 1  
SQ SEQUENCE 318 AA; 36997 MW; C88102EA1CAC1506 CRC64;

Query Match 92.7%; Score 89; DB 13; Length 318;

Best Local Similarity 94.4%; Pred. No. 5.8e-06;

Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 VIFNYKGNVLINKDIRC 18

|||||||

Db 45 VIFNYKGNHLINKDIRC 62

RESULT 2

Q9U6S0  
 ID Q9U6S0 PRELIMINARY; PRT; 421 AA.  
 AC Q9U6S0;  
 DT 01-MAY-2000 (TRENBLrel. 13, Created)  
 DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)  
 DT 01-JUN-2001 (TRENBLrel. 17, Last annotation update)  
 DE CALRETTICULIN PRECURSOR.  
 GN CALRET.  
 OS Strongylocentrotus purpuratus (Purple sea urchin).  
 OC Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;  
 OC Echinoida; Euechinoidea; Echinacea; Echinoida; Strongylocentrotidae;  
 OC Strongylocentrotus.  
 OX NCBI\_TaxID:7668;  
 RN [1]  
 RP SKOUNHCE FROM N.A.  
 RA SUNAN J.M., Just M.L., Lennarz W.J.;  
 RT "Cloning and Characterization of AlphaP Integrin and Calreticulin in  
 RT Embryos of the Sea Urchin."  
 RL Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AF177915; AAD55725.1; -;  
 DR InterPro; IPR000886; ER\_target.  
 DR InterPro; IPR001580; Calreticulin.  
 DR Pfam; PF00262; calreticulin; 1.  
 DR PRINTS; PR00626; CALRETTICULIN.  
 DR ProDom; PD001866; CALRETTICULIN; 1.  
 DR PROSITE; PS00804; CALRETTICULIN\_2; 1.  
 DR PROSITE; PS00805; CALRETTICULIN\_REPEAT; 3.  
 DR PROSITE; PS00014; ER\_TARGET; UNKNOWN\_1.  
 KW Signal.  
 FT SIGNAL 1 19 POTENTIAL.  
 FT CHAIN 20 421 CALRETTICULIN.  
 SQ SEQUENCE 421 AA; 48822 MW; 172C664F59F41F93 CRC64;

Query Match 90.6%; Score 87; DB 5; Length 421;  
 Best Local Similarity 88.9%; Pred. No. 1.6e-05;  
 Matches 16; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 VIFNYGKKNVLINKDIRC 18  
 DB 145 VIFNYGKKNLLKKDIRC 162

RESULT 3  
 ID Q26268 PRELIMINARY; PRT; 405 AA.  
 AC Q26268;  
 DT 01-NOV-1996 (TRENBLrel. 01, Created)  
 DT 01-NOV-1996 (TRENBLrel. 01, Last sequence update)  
 DT 01-JUN-2001 (TRENBLrel. 17, Last annotation update)  
 DE CALRETTICULIN.  
 OS Aplysia californica (California sea hare).  
 OC Eukaryota; Metazoa; Mollusca; Gastropoda; Opisthobranchia; Anaspidae;  
 OC Aplysiidae; Aplysia.  
 OX NCBI\_TaxID:6500;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA MEDLINE 93098937; PubMed 1463604;  
 RA Kennedy T.E., Kuhl D., Barzilai A., Sweatt J.D., Kandel E.R.;  
 RT "Long-term sensitization training in Aplysia leads to an increase in  
 RT calreticulin, a major presynaptic calcium-binding protein.";  
 RL Neuron 9:1013-1024(1992).  
 DR EMBL; S51239; AAB24569.1; -;  
 DR InterPro; IPR000886; ER\_target.  
 DR InterPro; IPR001580; Calreticulin.  
 DR Pfam; PF00262; calreticulin; 1.  
 DR PRINTS; PR00626; CALRETTICULIN.  
 DR ProDom; PD001866; Calreticulin; 1.  
 DR PROSITE; PS00803; CALRETTICULIN\_1; 1.  
 DR PROSITE; PS00804; CALRETTICULIN\_2; 1.  
 DR PROSITE; PS00805; CALRETTICULIN\_REPEAT; 3.  
 DR PROSITE; PS00014; ER\_TARGET; UNKNOWN\_1.  
 SQ SEQUENCE 405 AA; 46738 MW; 14CAA201840D1D69 CRC64;

Query Match 89.6%; Score 86; DB 5; Length 405;  
 Best Local Similarity 83.3%; Pred. No. 2.1e-05;  
 Matches 15; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 1 VIFNYGKKNVLINKDIRC 18  
 DB 142 VIFNYGKKNLLKKDIRC 159

RESULT 4  
 ID Q16893 PRELIMINARY; PRT; 410 AA.  
 AC Q16893;  
 DT 01-NOV-1996 (TRENBLrel. 01, Created)  
 DT 01-JAN-1999 (TRENBLrel. 09, Last sequence update)  
 DT 01-JUN-2001 (TRENBLrel. 17, Last annotation update)  
 DE CALRETTICULIN.  
 GN CRT-1.  
 OS Amblyomma americanum.  
 OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Acari;  
 OC Parasitiformes; Ixodida; Ixodidae; Amblyomma.  
 OX NCBI\_TaxID:6943;  
 RN [1]  
 RP SEQUENCE OF 49-410 FROM N.A.  
 RC TISSUE-SALIVARY GLANDS;  
 RA Jaworski D.C., Simmen F.A., Lamoreaux W.J., Coons L.B., Muller M.T.,  
 RA Needham G.R.;  
 RT "A secreted calreticulin protein in Ixodid tick (Amblyomma americanum)  
 RT saliva.";  
 RL J. Insect Physiol. 41:369-375(1995).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE-SALIVARY GLANDS;  
 RA Jaworski D.C.;  
 RL Submitted (MAR-1994) to the EMBL/GenBank/DBJ databases.  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE-SALIVARY GLANDS;  
 RA Fain-Thornton J.M., Jaworski D.C., Needham G.R.;  
 RL Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; U07708; AAC79094.1; -;  
 DR InterPro; IPR000886; ER\_target.  
 DR InterPro; IPR001580; Calreticulin.  
 DR Pfam; PF00262; calreticulin; 1.  
 DR PRINTS; PR00626; CALRETTICULIN.  
 DR ProDom; PD001866; Calreticulin; 1.  
 DR PROSITE; PS00803; CALRETTICULIN\_1; 1.  
 DR PROSITE; PS00805; CALRETTICULIN\_REPEAT; 3.  
 DR PROSITE; PS00014; ER\_TARGET; UNKNOWN\_1.  
 SQ SEQUENCE 410 AA; 47485 MW; 32CCB8750A17DC54 CRC64;

Query Match 88.5%; Score 85; DB 5; Length 410;  
 Best Local Similarity 88.9%; Pred. No. 3.1e-05;  
 Matches 16; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 VIFNYGKKNVLINKDIRC 18  
 DB 145 VIFNYGKKNLLKKDIRC 162

RESULT 5  
 ID Q9U916 PRELIMINARY; PRT; 406 AA.  
 AC Q9U916;  
 DT 01-MAY-2000 (TRENBLrel. 13, Created)  
 DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)  
 DT 01-JUN-2001 (TRENBLrel. 17, Last annotation update)  
 DE CALRETTICULIN.  
 GN CRC OR CG9429.  
 OS Drosophila melanogaster (Fruit fly).



OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;  
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
 OC Ephydroidea; Drosophilidae; Drosophila.  
 OX NCBI\_TaxID=7227;  
 RN [1]  
 RP SEQUENCE FROM N.A.

RC STRAIN-OREGON-R;  
 RA Dodo K., Sakoyama Y., Gamo S.;  
 RT "Drosophila melanogaster calreticulin for mRNA."  
 RL Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AB000718; BAA85379.1; -  
 DR FlyBase: FBgn0005585; Crc.  
 DR InterPro: IPR001580; Calreticulin.  
 DR InterPro: IPR000886; ER\_target.  
 DR Pfam: PF00262; calreticulin; 1.  
 DR PRINTS: PR00626; CALRETICULIN.  
 DR ProDom: PD001866; Calreticulin; 1.  
 DR PROSITE: PS00803; CALRETICULIN\_1; 1.  
 DR PROSITE: PS00804; CALRETICULIN\_2; 1.  
 DR PROSITE: PS00805; CALRETICULIN\_REPEAT; 3.  
 DR PROSITE: PS00014; ER\_TARGET; UNKNOWN\_1.  
 SQ SEQUENCE 406 AA; 46809 MW; 68BA49A6B81CC427 CRC64;

Query Match 82.3%; Score 79; DB 5; Length 406;  
 Best Local Similarity 83.3%; Pred. No. 0.00026;  
 Matches 15; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 VIFNYKGNVLINKDIRC 18  
 |||:|||||:|||||  
 Db 146 VIFSYGKNHLISKDIRC 163

RESULT 6  
 Q98984  
 ID Q98984 PRELIMINARY; PRT; 419 AA.  
 DT 01-FEB-1997 (TREMBLrel. 02, Created)  
 DT 01-FEB-1997 (TREMBLrel. 02, Last sequence update)  
 DE 01-JUN-2001 (TREMBLrel. 17, Last annotation update)  
 DE CALRETICULIN.  
 OS Rana rugosa (Frog).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Ranidae; Rana.  
 OX NCBI\_TaxID=8410;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE-96234004; PubMed-8654561;  
 RA Yamamoto S., Nakamura M.;  
 RT "Calnexin: its molecular cloning and expression in the liver of the  
 RT frog, Rana rugosa."  
 RL FEBS Lett. 387:27-32(1996).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RA Yamamoto S.;  
 RT "Strong expression of the calreticulin gene in the liver of Rana  
 RT rugosa Tadpoles."  
 RL J. Exp. Zool. 0:0-0(1996).  
 DR EMBL: D78589; BAA11425.1; -  
 DR InterPro: IPR000886; ER\_target.  
 DR InterPro: IPR001580; Calreticulin.  
 DR Pfam: PF00262; calreticulin; 1.  
 DR PRINTS: PR00626; CALRETICULIN.  
 DR ProDom: PD001866; Calreticulin; 1.  
 DR PROSITE: PS00803; CALRETICULIN\_1; 1.  
 DR PROSITE: PS00804; CALRETICULIN\_2; 1.  
 DR PROSITE: PS00805; CALRETICULIN\_REPEAT; 3.  
 DR PROSITE: PS00014; ER\_TARGET; UNKNOWN\_1.  
 SQ SEQUENCE 419 AA; 48658 MW; 2C857036769673BF CRC64;

Query Match 81.2%; Score 78; DB 13; Length 419;  
 Best Local Similarity 88.2%; Pred. No. 0.00038;

Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
 Qy 1 VIFNYKGNVLINKDIR 17  
 |||:|||||:|||||  
 Db 147 VIFNYKGNLQINKDIR 163

RESULT 7  
 Q9PUC1  
 ID Q9PUC1 PRELIMINARY; PRT; 417 AA.  
 AC Q9PUC1;  
 DT 01-MAY-2000 (TREMBLrel. 13, Created)  
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)  
 DE 01-JUN-2001 (TREMBLrel. 17, Last annotation update)  
 DE CALRETICULIN.  
 OS Brachydanio rerio (zebrafish) (zebra danio).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;  
 OC Cypriniformes; Cyprinidae; Rasborinae; Danio.  
 OX NCBI\_TaxID=7955;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Rubinstein A.L., Lee D., Luo R., Henion P.D., Halpern M.E.;  
 RT "Genes Dependent on Zebrafish cyclops Function Identified by AFLP  
 RT Differential Gene Expression Screen."  
 RL Genesis 0:0-0(1999).  
 DR EMBL: AF195882; AAF13700.1; -  
 DR InterPro: IPR000886; ER\_target.  
 DR InterPro: IPR001580; Calreticulin.  
 DR Pfam: PF00262; calreticulin; 1.  
 DR ProDom: PD001866; Calreticulin.  
 DR ProDom: PD001866; Calreticulin; 1.  
 DR PROSITE: PS00803; CALRETICULIN\_1; 1.  
 DR PROSITE: PS00804; CALRETICULIN\_2; 1.  
 DR PROSITE: PS00805; CALRETICULIN\_REPEAT; 3.  
 DR PROSITE: PS00014; ER\_TARGET; UNKNOWN\_1.  
 SQ SEQUENCE 417 AA; 48723 MW; 2000C5B4004699B6 CRC64;

Query Match 79.2%; Score 76; DB 13; Length 417;  
 Best Local Similarity 77.8%; Pred. No. 0.00077;  
 Matches 14; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 VIFNYKGNVLINKDIRC 18  
 |||:|||||:|||||  
 Db 146 VIFNYGQNHLLKKDKC 163

RESULT 8  
 O76961  
 ID O76961 PRELIMINARY; PRT; 403 AA.  
 AC O76961;  
 DT 01-NOV-1998 (TREMBLrel. 08, Created)  
 DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)  
 DE 01-JUN-2001 (TREMBLrel. 17, Last annotation update)  
 DE CALRETICULIN PRECURSOR.  
 GN CRT.  
 OS Necator americanus.  
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Strongylida;  
 OC Ancylostomatidae; Ancylostomatidae; Bunostominae; Necator.  
 OX NCBI\_TaxID=51031;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Pritchard D.I., Brown A., McElroy P., Loukas A., Girdwood K.,  
 RA Berry C., Fullkrug R., Beck E.;  
 RT "Calreticulin is a hookworm allergen."  
 RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AJ006790; CAA07254.1; -  
 DR InterPro: IPR000886; ER\_target.  
 DR InterPro: IPR001580; Calreticulin.  
 DR Pfam: PF00262; calreticulin; 1.  
 DR PRINTS: PR00626; CALRETICULIN.  
 DR ProDom: PD001866; Calreticulin; 1.

DR PROSITE; PS00803; CALRETICULIN\_1; 1.  
 DR PROSITE; PS00804; CALRETICULIN\_2; 1.  
 DR PROSITE; PS00805; CALRETICULIN\_REPEAT; 3.  
 DR PROSITE; PS00014; ER\_TARGET; UNKNOWN\_1.  
 KW Signal; Allergen.  
 FT SIGNAL 1 16 POTENTIAL.  
 SQ SEQUENCE 403 AA; 46833 MW; 21F38B0515487B6F CRC64;

Query Match 77.1%; Score 74; DB 5; Length 403;  
 Best Local Similarity 82.4%; Pred. No. 0.0015;  
 Matches 14; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
 QY 2 IFNYKGNVNLINKDIRC 18  
 DB 143 IFNYKGNVNLINKDIRC 159  
 ||:|||||:|:|||||

RESULT 9  
 Q91711 PRELIMINARY; PRT; 343 AA.  
 ID Q91711; TREMBLrel. 05, Created)  
 DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)  
 DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)  
 DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)  
 DE CALRETICULIN (FRAGMENT).  
 OS Xenopus laevis (African clawed frog).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;  
 OC Xenopodidae; Xenopus.  
 ON NCBI\_TaxID 8355;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE: BRAIN;  
 RX MEDLINE 93074997; PubMed 1445218;  
 TX Treves S., Zorzato F., Pozzan T.;  
 RT Identification of calreticulin isoforms in the central nervous  
 system.";  
 RL Blochm., J. 287:579-581(1992).  
 DR EMBL; X67598; CAA47867.1; -.  
 DR InterPro; IP0001580; Calreticulin.  
 DR Pfam; PF00262; calreticulin; 1.  
 DR PRINTS; PR00626; CALRETICULIN.  
 DR PRODOM; PD001866; Calreticulin; 1.  
 DR PROSITE; PS00803; CALRETICULIN\_1; 1.  
 DR PROSITE; PS00804; CALRETICULIN\_2; 1.  
 DR PROSITE; PS00805; CALRETICULIN\_REPEAT; 3.  
 FT NON\_TER 1 343  
 SQ SEQUENCE 343 AA; 40105 MW; 3E7DDAFA33B91DE1 CRC64;

Query Match 76.0%; Score 73; DB 13; Length 343;  
 Best Local Similarity 77.8%; Pred. No. 0.0018;  
 Matches 14; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 VIFNYKGNVNLINKDIRC 18  
 DB 118 VIFQYKKNLQINKDIRC 135  
 ||| || ||: |||||  
 RESULT 10  
 O18478 PRELIMINARY; PRT; 375 AA.  
 ID O18478;  
 DT 01-JAN-1998 (TREMBLrel. 05, Created)  
 DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)  
 DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)  
 DE RAL-1 PROTEIN (FRAGMENT).  
 OS Litomosoides sigmodontis.  
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Spirurida; Filarioidea;  
 OC Onchocercidae; Litomosoides.  
 ON NCBI\_TaxID 42156;

RN SEQUENCE FROM N.A.  
 RP MacLennan K., Hoffman W.H., Taylor D.W.;  
 RL Submitted (SEP-1997) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AJ001621; CAA04877.1; -.  
 DR InterPro; IP0001580; Calreticulin.  
 DR Pfam; PF00262; calreticulin; 1.  
 DR PRINTS; PR00626; CALRETICULIN.  
 DR PRODOM; PD001866; Calreticulin; 1.  
 DR PROSITE; PS00803; CALRETICULIN\_1; 1.  
 DR PROSITE; PS00804; CALRETICULIN\_2; 1.  
 DR PROSITE; PS00805; CALRETICULIN\_REPEAT; 3.  
 FT NON\_TER 375 375  
 SQ SEQUENCE 375 AA; 43842 MW; 03F7642FBFF7A5B8 CRC64;

Query Match 76.0%; Score 73; DB 5; Length 375;  
 Best Local Similarity 72.2%; Pred. No. 0.002;  
 Matches 13; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 VIFNYKGNVNLINKDIRC 18  
 DB 144 VIFHYKGRNHHMKKDIRC 161  
 |||:||||:|:|||||

RESULT 11  
 O97372 PRELIMINARY; PRT; 387 AA.  
 ID O97372; TREMBLrel. 10, Created)  
 DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)  
 DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)  
 DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)  
 DE CALRETICULIN PRECURSOR.  
 OS Dirofilaria immitis.  
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Spirurida; Filarioidea;  
 OC Onchocercidae; Dirofilaria.  
 ON NCBI\_TaxID-6287;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE-99094497; PubMed-9879888;  
 RA Tsuji N., Morales T.H., Ozols V.V., Carmody A.B., Chandrashekar R.;  
 RT "Molecular characterization of a calcium-binding protein from the  
 filarial parasite Dirofilaria immitis.";  
 RL Mol. Biochem. Parasitol. 97:69-79(1998).  
 DR EMBL; AF052978; AAD03405.1; -.  
 DR InterPro; IP0001580; Calreticulin.  
 DR Pfam; PF00262; calreticulin; 1.  
 DR PRINTS; PR00626; CALRETICULIN.  
 DR PRODOM; PD001866; Calreticulin; 1.  
 DR PROSITE; PS00803; CALRETICULIN\_1; 1.  
 DR PROSITE; PS00804; CALRETICULIN\_2; 1.  
 DR PROSITE; PS00805; CALRETICULIN\_REPEAT; 3.  
 KW Signal.  
 FT SIGNAL 1 18 POTENTIAL.  
 FT CHAIN 19 387 CALRETICULIN.  
 SQ SEQUENCE 387 AA; 44941 MW; E7741BF6AFA5885 CRC64;

Query Match 76.0%; Score 73; DB 5; Length 387;  
 Best Local Similarity 72.2%; Pred. No. 0.0021;  
 Matches 13; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 VIFNYKGNVNLINKDIRC 18  
 DB 144 VIFHYKGRNHHMKKDIRC 161  
 |||:||||:|:|||||  
 RESULT 12  
 Q91710 PRELIMINARY; PRT; 411 AA.  
 ID Q91710; TREMBLrel. 05, Created)  
 DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)  
 DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)

Query Match	75.0%	Score 72:	DB 5;	Length 350;
Best Local Similarity	77.8%	Pred. No.	0.0027;	
Matches	14;	Conservative	1;	Mismatches 3; Indels 0; Gaps 0;

  

QY	1	VIFNYGKGNVLINKDIRC 18
		:
Db	99	VIFNYGKGNHLIKKDIPC 116

  

RESULT	14
O45034	PRELIMINARY; PRT; 396 AA.
ID	O45034
AC	O45034;
DT	01-JUN-1998 (TrEMBLrel. 06, Created)
DT	01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
DT	01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE	CALRETICULIN.
OS	Schistosoma japonicum (Blood fluke).
OC	Eukaryota; Metazoa; Platyhelminthes; Rhabditophora; Neodermata;
OC	Trematoda; Digenea; Strigeldida; Schistosomatoidea; Schistosomatidae;
OC	Schistosoma.
OX	NCBI_TaxID=6182;
RN	[1]
RP	SEQUENCE FROM N.A.
RC	STRAIN=PHILIPPINE (MINDORO);
RA	Scott J.C.;
RL	Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
DR	EMBL; AF044408; AAC00515.1; -
DR	InterPro; IPR000886; ER_target.
DR	InterPro; IPR001580; Calreticulin.
DR	Pfam; PF00262; calreticulin; 1.
DR	PRINTS; PR00626; CALRETICULIN.
DR	ProDom; PD001866; Calreticulin; 1.
DR	PROSITE; PS00803; CALRETICULIN_1; 1.
DR	PROSITE; PS00804; CALRETICULIN_2; 1.
DR	PROSITE; PS00805; CALRETICULIN_REPEAT; 2.
DR	PROSITE; PS00014; ER_TARGET; UNKNOWN_1.
SQ	SEQUENCE 396 AA; 45813 MW; C57394C6FB4CD77B CRC64;

  

Query Match	75.0%	Score 72:	DB 5;	Length 396;
Best Local Similarity	77.8%	Pred. No.	0.003;	
Matches	14;	Conservative	1;	Mismatches 3; Indels 0; Gaps 0;

  

QY	1	VIFNYGKGNVLINKDIRC 18
		:
Db	145	VIFNYGKGNHLIKKDIPC 162

  

RESULT	15
Q9U5G0	PRELIMINARY; PRT; 321 AA.
ID	Q9U5G0
AC	Q9U5G0;
DT	01-MAY-2000 (TrEMBLrel. 13, Created)
DT	01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT	01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE	CALRETICULIN (FRAGMENT).
OS	Eptatretus burgeri (Inshore hagfish).
OC	Eukaryota; Metazoa; Chordata; Craniata; Hyperotreti; Myxiniformes;
OC	Myxiniidae; Eptatretinae; Eptatretus.
OX	NCBI_TaxID=7764;
RN	[1]
RP	SEQUENCE FROM N.A.
RC	TISSUE=LIVER;
RX	MEDLINE=20063780; PubMed=10594174;
RT	Kuraku S., Hoshiyama D., Katoh K., Suga H., Miyata T.;
RT	"Monophyly of lampreys and hagfishes supported by nuclear DNA-coded
RT	genes";
RL	J. Mol. Evol. 49:729-735(1999).
DR	EMBL; AB025323; BAA88476.1; -
DR	InterPro; IPR000886; ER_target.
DR	InterPro; IPR001580; Calreticulin.

DR pfam: PF00262; calreticulin; 1.  
 DR PRINTS; PR00626; CALRETICULIN.  
 DR ProDom; PD001866; Calreticulin; 1.  
 DR PROSITE; PS00804; CALRETICULIN\_2; 1.  
 DR PROSITE; PS00805; CALRETICULIN\_REPEAT; 3.  
 DR PROSITE; PS00014; ER\_TARGET; UNKNOWN\_1.  
 FT NON\_TER 1  
 SQ SEQUENCE 321 AA; 37367 MW; 6E8DFA98D42F7AEF CRC64;

Query Match 62.5%; Score 60; DB 13; Length 321;  
 Best Local Similarity 61.1%; Pred. No. 0.18;  
 Matches 11; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 VIFNYGKNVLINKDIRC 18  
 ||| |||| ||| :||  
 Db 45 VILNSKGNHLIKKEVKC 62

Search completed: January 9, 2002, 15:03:29  
 Job time: 271 sec

GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: January 9, 2002, 15:12:15 ; Search time 25.18 Seconds  
(without alignments)  
26.210 Million cell updates/sec

Title: US-09-828-000-6

Perfect score: 96

Sequence: 1 VIFNYKGNVLINKDIRC 18

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 100059 seqs, 36664827 residues

Total number of hits satisfying chosen parameters: 100059

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt\_39:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	96	100.0	400	1 CRT1_BOVIN	P52193 bos taurus
2	96	100.0	416	1 CRTC_MOUSE	P14211 mus musculus
3	96	100.0	416	1 CRTC_RAT	P18418 rattus norv
4	96	100.0	417	1 CRTC_HUMAN	P27797 homo sapien
5	96	100.0	418	1 CRTC_RABIT	P15253 oryctolagus
6	96	100.0	421	1 CRT2_BOVIN	P42918 bos taurus
7	79	82.3	406	1 CRTC_DROME	P29413 drosophila
8	72	75.0	393	1 CRTC_SCHMA	Q06814 schistosoma
9	66	68.8	388	1 RALI_ONCVO	P11012 onchocerca
10	64	66.7	395	1 CRTC_CAEEL	P27798 caenorhabdi
11	61	63.5	420	1 CRTC_CHLRE	Q9std3 chlamydomon
12	59	61.5	424	1 CRTC_DICDI	Q23858 dictyosteli
13	53	55.2	401	1 CRTC_EUGGR	Q92ny3 euglena gra
14	53	55.2	416	1 CRTC_BETVU	O81919 beta vulgar
15	52	54.2	424	1 CRT3_ARATH	O04153 arabidopsis
16	51	53.1	725	1 NCA2_MOUSE	P13594 mus musculus
17	51	53.1	761	1 NCA2_HUMAN	P13592 homo sapien
18	51	53.1	848	1 NCA1_HUMAN	P13591 homo sapien
19	51	53.1	853	1 NCA1_BOVIN	P31836 bos taurus
20	51	53.1	858	1 NCA1_RAT	P13596 rattus norv
21	51	53.1	1091	1 NCA1_CHICK	P13590 gallus gall
22	51	53.1	1115	1 NCA1_MOUSE	P13595 mus musculus
23	48	50.0	421	1 CRTC_PRUAR	Q9xf98 prunus arne
24	48	50.0	424	1 CRT2_ARATH	Q38858 arabidopsis
25	48	50.0	463	1 VDMA_CHICK	Q90578 gallus gall
26	47	49.0	1088	1 NCA1_XENLA	P16170 xenopus lae
27	47	49.0	1092	1 NCA2_XENLA	P63335 xenopus lae
28	44	45.8	417	1 PGK_METJA	Q58058 methanococc
29	44	45.8	420	1 CRTC_MAIZE	Q9sp22 zea mays
30	44	45.8	424	1 CRTC_ORISA	Q9sl98 oryza sativ
31	44	45.8	425	1 CRT1_ARATH	O04151 arabidopsis
32	44	45.8	496	1 CHK1_SCHPO	P34208 schizosacch
33	43	44.8	327	1 RPOA_UREPA	Q9pqn4 ureaplasma

#### ALIGNMENTS

RESULT 1

CRT1\_BOVIN  
ID CRT1\_BOVIN STANDARD; PRT; 400 AA.  
AC P52193;  
DT 01-OCT-1996 (Rel. 34, Created)  
DT 01-OCT-1996 (Rel. 34, Last sequence update)  
DT 01-OCT-1996 (Rel. 34, Last annotation update)  
DE CALRETICULIN, BRAIN ISOFORM 1 (CRP55) (CALREGULIN) (HACBP).  
OS Bos taurus (Bovine).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
OC Bovidae; Bovinae; Bos.  
OX NCBI\_TaxID=9913;  
RN [1]  
RP SEQUENCE.  
RC TISSUE=Brain;  
RX MEDLINE=94183174; PubMed=8135753;  
RA Matsuoka K., Seta K., Yamakawa Y., Okuyama T., Shinoda T., Isobe T.;  
RT "Covalent structure of bovine brain calreticulin.";  
RL Biochem. J. 298:435-442(1994).  
CC -!- FUNCTION: THIS PROTEIN BINDS CALCIUM. THERE ARE BOTH HIGH AND LOW AFFINITY CALCIUM-BINDING SITES.  
CC -!- SUBUNIT: MONOMER.  
CC -!- SUBCELLULAR LOCATION: ENDOPLASMIC RETICULUM LUMEN.  
CC -!- SIMILARITY: BELONGS TO THE CALRETICULIN FAMILY.  
DR InterPro: IPR001580; Calreticulin.  
DR InterPro: IPR000886; ER\_target.  
DR Pfam: PF00262; calreticulin; 1.  
DR PRINTS: PR00626; CALRETICULIN.  
DR ProDom: PD001866; Calreticulin; 1.  
DR PROSITE: PS00014; ER\_TARGET; 1.  
DR PROSITE: PS00803; CALRETICULIN\_1; 1.  
DR PROSITE: PS00804; CALRETICULIN\_2; 1.  
DR PROSITE: PS00805; CALRETICULIN\_REPEAT; 3.  
KW Endoplasmic reticulum; Calcium-binding; Repeat; Glycoprotein.  
FT DOMAIN 1 180 N-DOMAIN.  
FT DOMAIN 181 291 P-DOMAIN.  
FT DOMAIN 292 400 C-DOMAIN.  
FT DOMAIN 174 238 4 X APPROXIMATE REPEATS.  
FT REPEAT 174 185 1-1.  
FT REPEAT 193 204 1-2.  
FT REPEAT 210 221 1-3.  
FT REPEAT 227 238 1-4.  
FT REPEAT 242 280 3 X APPROXIMATE REPEATS.  
FT REPEAT 242 252 2-1.  
FT REPEAT 256 266 2-2.  
FT REPEAT 270 280 2-3.  
FT DOMAIN 334 390 ASP/GLU/LYS-RICH.  
FT DISULFID 120 146  
FT CARBOHYD 162 162  
FT SITE 397 400 N-LINKED (GLCNAC. . .).  
SQ SEQUENCE 400 AA; 46381 MW; 7DB68DFC689EEF1 CRC64;  
PREVENT SECRETION FROM ER (POTENTIAL).

Query Match 100.0%; Score 96; DB 1; Length 400;  
Best Local Similarity 100.0%; Pred. No. 1.3e-07;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VIFNYGKNVINKDIRC 18  
 DB 129 VIFNYGKNVINKDIRC 146

RESULT 2  
 CRTCL\_MOUSE STANDARD; PRT; 416 AA.

AC P14211;  
 DT 01-JAN-1990 (Rel. 13, Created)  
 DT 01-JAN-1990 (Rel. 13, Last sequence update)  
 DT 15-DEC-1998 (Rel. 37, Last annotation update)  
 DR CALRETICULIN PRECURSOR (CRP55) (CALREGULIN) (HACBP) (ERP60).  
 GN CALR.

OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID:10090;  
 RN [1]

SEQUENCE FROM N.A., AND SEQUENCE OF 18-48 AND 129-161.  
 RC STRAIN BALB/C; TISSUE=Liver;  
 RX MEDLINE 90059955; PubMed:2583110;  
 RA Smith M.J., Koch G.L.E.;  
 RT "Multiple zones in the sequence of calreticulin (CRP55, calregulin, HACBP), a major calcium binding ER/SR protein.";  
 RL EMBO J. 8:3581-3586(1989).  
 RN [2]

SEQUENCE FROM N.A.  
 RX MEDLINE 93013037; PubMed 1398135;  
 RA Mazzarella R.A., Gold P., Cunningham M., Green M.;  
 RT "Determination of the sequence of an expressible cDNA clone encoding Exp60/calregulin by the use of a novel nested set method.";  
 RL Gene 120:217-225(1992).  
 RN [3]

SEQUENCE OF 18-38.  
 RC TISSUE=Fibroblast;  
 RX MEDLINE 95009907; PubMed 7523108;  
 RA Merrick H.A., Patterson R.M., Wichter L.L., He C., Selkirk J.K.;  
 RT "Separation and sequencing of familial and novel murine proteins using preparative two-dimensional gel electrophoresis.";  
 RL Electrophoresis 15:735-745(1994).  
 RN [1]

FUNCTION: THIS PROTEIN BINDS CALCIUM. THERE ARE BOTH HIGH AND LOW AFFINITY CALCIUM-BINDING SITES.  
 CC -1 SURFINT: MONOMER (BY SIMILARITY).  
 CC -1 SUBCELLULAR LOCATION: ENDOPLASMIC RETICULUM LUMEN.  
 CC -1 SIMILARITY: BELONGS TO THE CALRETICULIN FAMILY.

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EMBL; X14946; CAA33053.1; -.  
 EMBL; M92988; AAA37569.1; -.  
 PIR; S06763; S06763.  
 PIR; JC1444; JC1444.  
 SWISS-2DPAGE; P14211; MOUSE.  
 MGD; MGI:88252; Calr.

InterPro; IPR001580; Calreticulin.  
 InterPro; IPR000886; ER\_target.  
 Pfam; PF00262; calreticulin\_1.  
 PRINTS; PR00626; CALRETICULIN.  
 PRODOM; PD001866; Calreticulin.  
 PROSITE; PS00014; ER\_TARGET; 1.  
 PROSITE; PS00803; CALRETICULIN\_1; 1.  
 PROSITE; PS00804; CALRETICULIN\_2; 1.  
 PROSITE; PS00805; CALRETICULIN\_REPEAT; 3.  
 Endoplasmic reticulum; Calcium-binding; Repeat; Signal.

FT SIGNAL 1 17  
 FT CHAIN 18 416  
 FT DOMAIN 18 197  
 FT DOMAIN 198 308  
 FT DOMAIN 309 416  
 FT DOMAIN 191 255  
 FT REPEAT 191 202  
 FT REPEAT 210 221  
 FT REPEAT 227 238  
 FT REPEAT 244 255  
 FT DOMAIN 259 297  
 FT REPEAT 259 269  
 FT REPEAT 273 283  
 FT REPEAT 287 297  
 FT DOMAIN 351 407  
 FT DISULFID 137 163  
 FT SITE 413 416  
 SQ SEQUENCE 416 AA; 47994 MW; 24C03B00913408D8 CRC64;

Query Match 100.0%; Score 96; DB 1; Length 416;  
 Best Local Similarity 100.0%; Pred. NO. 1.4e-07;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VIFNYGKNVINKDIRC 18  
 DB 146 VIFNYGKNVINKDIRC 163

RESULT 3  
 CRTCL\_MOUSE STANDARD; PRT; 416 AA.

AC P18418; P10452;  
 DT 01-MAR-1989 (Rel. 10, Created)  
 DT 01-NOV-1990 (Rel. 16, Last sequence update)  
 DT 01-NOV-1997 (Rel. 35, Last annotation update)  
 DE CALRETICULIN PRECURSOR (CRP55) (CALREGULIN) (HACBP) (ERP60) (CALBP)  
 DE (CALCIUM-BINDING PROTEIN 3) (CABP3).  
 GN CALR.

Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 OX NCBI\_TaxID:10116;  
 RN [1]

SEQUENCE FROM N.A.  
 RC STRAIN=SPRAGUE-DAWLEY; TISSUE=Brain cortex;  
 RX MEDLINE-90370496; PubMed:2395661;  
 RA Murthy K.K., Banville D., Srikant C.B., Carrier F., Bell A.,  
 RA Holmes C., Patel Y.C.;  
 RT "Structural homology between the rat calreticulin gene product and the Onchocerca volvulus antigen Rai-1.";  
 RL Nucleic Acids Res. 18:4933-4933(1990).  
 RN [2]

SEQUENCE FROM N.A.  
 RC STRAIN=SPRAGUE-DAWLEY;  
 RX MEDLINE-93202172; PubMed:8453984;  
 RA Nakamura M., Moriya M., Baba T., Michikawa Y., Yamanobe T., Arai K.,  
 RA Okinaga S., Kobayashi T.;  
 RT "An endoplasmic reticulum protein, calreticulin, is transported into the acrosome of rat sperm.";  
 RL Exp. Cell Res. 205:101-110(1993).  
 RN [3]

SEQUENCE FROM N.A.  
 RC STRAIN=SPRAGUE-DAWLEY; TISSUE=Liver;  
 RX MEDLINE-95181573; PubMed:7876339;  
 RA Soennichsen B., Fuelekruug J., van Nguyen P., Diekmann W.,  
 RA Robinson D.G., Mieskes G.;  
 RT "Retention and retrieval: both mechanisms cooperate to maintain calreticulin in the endoplasmic reticulum.";  
 RL J. Cell Sci. 107:2705-2717(1994).  
 RN [4]

SEQUENCE OF 270-358 FROM N.A.  
 RC STRAIN=SPRAGUE-DAWLEY;

RA Lone Y.C., Bailly A., Latruffe N.;  
RL Submitted (DEC-1988) to the EMBL/GenBank/DBJ databases.  
RN [5]  
RX SEQUENCE OF 18-29.  
RX MEDLINE=91054414; PubMed=2241926;  
RA Treves S., de Mattei M., Lanfredi M., Villa A., Green N.M.,  
RA MacLennan D.H., Meldolesi J., Pozzan T.;  
RT "Calreticulin is a candidate for a calsequestrin-like function in  
RT Ca2(+)-storage compartments (calciosomes) of liver and brain.";  
RL Biochem. J. 271:473-480(1990).  
RN [6]  
RP SEQUENCE OF 18-32.  
RC STRAIN=SPRAGUE-DAWLEY; TISSUE=Testis;  
RX MEDLINE=92360010; PubMed=1497655;  
RA Nakamura M., Michikawa Y., Baba T., Okinaga S., Arai K.;  
RT "Calreticulin is present in the acrosome of spermatids of rat  
RT testis.";  
RL Biochem. Biophys. Res. Commun. 186:668-673(1992).  
RN [7]  
RP SEQUENCE OF 18-32.  
RC STRAIN=LEC; TISSUE=Liver;  
RX MEDLINE=94072621; PubMed=8251535;  
RA Yokoi T., Nagayama S., Kajiwara R., Kawaguchi Y., Horiuchi R.,  
RA Kanataki T.;  
RT "Identification of protein disulfide isomerase and calreticulin as  
RT autoimmune antigens in LEC strain of rats.";  
RL Biochim. Biophys. Acta 1158:339-344(1993).  
CC !- FUNCTION: THIS PROTEIN BINDS CALCIUM. THERE ARE BOTH HIGH AND  
CC LOW AFFINITY CALCIUM-BINDING SITES.  
CC !- SUBUNIT: MONOMER (BY SIMILARITY).  
CC !- SUBCELLULAR LOCATION: ENDOPLASMIC RETICULUM LUMEN.  
CC !- SIMILARITY: BELONGS TO THE CALRETICULIN FAMILY.  
CC !- CAUTION: WAS ORIGINALLY (REF.2) THOUGHT TO BE D-BETA-  
CC HYDROXYBUTYRATE DEHYDROGENASE.  
CC -----  
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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC -----  
DR EMBL; D78308; BAA11345.1; .  
DR EMBL; X53363; CAA37446.1; .  
DR EMBL; X13702; CAA31987.1; ALT\_SEQ.  
DR EMBL; X79327; CAA55890.1; .  
DR PIR; S04867; S04867.  
DR PIR; S11205; S11205.  
DR PIR; S13045; S13045.  
DR PIR; A49176; A49176.  
DR PIR; S45036; S45036.  
DR PIR; JH0819; JH0819.  
DR InterPro; IPR001580; Calreticulin.  
DR InterPro; IPR000886; ER target.  
DR Pfam; PF00262; calreticulin; 1.  
DR PRINTS; P00626; CALRETICULIN.  
DR PRODOM; PD001866; Calreticulin; 1.  
DR PROSITE; PS00014; ER\_TARGET; 1.  
DR PROSITE; PS00803; CALRETICULIN\_1; 1.  
DR PROSITE; PS00804; CALRETICULIN\_2; 1.  
DR PROSITE; PS00805; CALRETICULIN\_REPEAT; 3.  
KW Endoplasmic reticulum; Calcium-binding; Repeat; Signal.  
FT SIGNAL 1 17  
FT CHAIN 18 416 CALRETICULIN.  
FT DOMAIN 18 197 N-DOMAIN.  
FT DOMAIN 198 308 P-DOMAIN.  
FT DOMAIN 309 416 C-DOMAIN.  
FT DOMAIN 191 255 4 X APPROXIMATE REPEATS.  
FT REPEAT 191 202 1-1.  
FT REPEAT 210 221 1-2.  
FT REPEAT 227 238 1-3.  
FT REPEAT 244 255 1-4.

FT DOMAIN 259 297 3 X APPROXIMATE REPEATS.  
FT REPEAT 259 269 2-1.  
FT REPEAT 273 283 2-2.  
FT REPEAT 287 297 2-3.  
FT DOMAIN 351 407 ASP/GLU/LYS-RICH.  
FT DISULFID 137 163 BY SIMILARITY.  
FT SITE 413 416 PREVENT SECRETION FROM ER.  
SQ SEQUENCE 416 AA; 47995 MW; 2E6713CED31A2970 CRC64;  
  
Query Match 100.0%; Score 96; DB 1; Length 416;  
Best Local Similarity 100.0%; Pred. No. 1.4e-07;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 VIFNYKGNVLINKDIRC 18  
Db 146 VIFNYKGNVLINKDIRC 163  
|||||  
  
RESULT 4  
ID CRTCT\_HUMAN STANDARD; PRT; 417 AA.  
AC P27797;  
DT 01-AUG-1992 (Rel. 23, Created)  
DT 01-AUG-1992 (Rel. 23, Last sequence update)  
DT 20-AUG-2001 (Rel. 40, Last annotation update)  
DE CALRETICULIN PRECURSOR (CRP55) (CALREGULIN) (HACBP) (ERP60) (52 KDA  
DE RIBONUCLEOPROTEIN AUTOANTIGEN RO/SS-A).  
GN CALR OR CRTCT.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
ON NCBI\_TaxID=9606;  
RX [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=92013129; PubMed=1919005;  
RA Rokeach L.A., Haselby J.A., Melloy F.F., Smeenk R.J., Unnasch T.R.,  
RA Greene B.M., Hoch S.O.;  
RT "Characterization of the autoantigen calreticulin.";  
RL J. Immunol. 147:3031-3039(1991).  
RN [2]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=902337213; PubMed=2332496;  
RA McCaulliffe D.P., Lux F.A., Lieu T.S., Sanz I., Hanke J., Newkirk M.M.,  
RA Bachinski L.L., Itoh Y., Siciliano M.J., Reichlin M., Sontheimer R.D.,  
RA Capra J.D.;  
RT "Molecular cloning, expression, and chromosome 19 localization of a  
RT human Ro/SS-A autoantigen.";  
RL J. Clin. Invest. 85:1379-1391(1990).  
RN [3]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=92129342; PubMed=1733953;  
RA McCaulliffe D.P., Yang Y.S., Wilson J., Sontheimer R.D., Capra J.D.;  
RT "The 5'-flanking region of the human calreticulin gene shares  
RT homology with the human GRP78, GRP94, and protein disulfide isomerase  
RT promoters.";  
RL J. Biol. Chem. 267:2557-2562(1992).  
RN [4]  
RP SEQUENCE FROM N.A.  
RA Lamerdin J., McCreedy P., Stilwagen S., Ramirez M., Carrano A.;  
RL Submitted (MAR-1997) to the EMBL/GenBank/DBJ databases.  
RN [5]  
RP SEQUENCE OF 18-36.  
RX MEDLINE=92002034; PubMed=1911778;  
RA Rojiani M.V., Finlay B.B., Gray V., Dedhar S.;  
RT "In vitro interaction of a polypeptide homologous to human Ro/SS-A  
RT antigen (calreticulin) with a highly conserved amino acid sequence in  
RT the cytoplasmic domain of integrin alpha subunits.";  
RL Biochemistry 30:9859-9866(1991).  
RN [6]  
RP SEQUENCE OF 18-32.  
RX MEDLINE=90380058; PubMed=2400400;  
RA Krause K.H., Simmerman H.K.B., Jones L.R., Campbell K.P.;

\*Sequence similarity of calreticulin with a Ca2(+)-binding protein that co-purifies with an Ins(1,4,5)P3-sensitive Ca2+ store in HL-60 cells.";  
 Biochem. J. 270:545-548(1990).  
 [7]

SEQUENCE OF 18-28.

TISSUE Liver;  
 MEDLINE-93162045; PubMed 1286669;  
 Hochstrasser D.F., Frutiger S., Paquet N., Bairoch A., Ravier F., Pasquelli C., Sanchez J.-C., Tissot J.-D., Bjellqvist B., Vargas R., Appel R.D., Hughes G.J.;  
 "Human liver protein map: a reference database established by microsequencing and gel comparison.";  
 Electrophoresis 13:982-1001(1992).  
 [8]

PARTIAL SEQUENCE OF 25-34; 56-62; 208-221 AND 273-278.

TISSUE-Keratinocytes;

MEDLINE-93162043; PubMed 1286667;

Rammason H.H., Van Damme J., Puype M., Gessner B., Celis J.E., Vandenkerckhove J.;

\*Microsequences of 145 proteins recorded in the two-dimensional gel protein database of normal human epidermal keratinocytes.";  
 Electrophoresis 13:960-969(1992).  
 [9]

SEQUENCE OF 18-26.

TISSUE-Colon carcinoma;

MEDLINE 97295306; PubMed 9150948;

Ji H., Reid G.E., Moritz R.L., Eddes J.S., Burgess A.W., Simpson R.J.;

\*A two-dimensional gel database of human colon carcinoma proteins.";

Electrophoresis 18:605-613(1997).

- FUNCTION: THIS PROTEIN BINDS CALCIUM. THERE ARE BOTH HIGH AND

LOW AFFINITY CALCIUM-BINDING SITES.

- SUBUNIT: MONOMER (BY SIMILARITY).

- SUBCELLULAR LOCATION: ENDOPLASMIC RETICULUM LUMEN.

- SIMILARITY: BELONGS TO THE CALRETICULIN FAMILY.

- CAUTION: WAS ORIGINALLY (REF.2) THOUGHT TO BE THE RO AUTOANTIGEN.

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EMBL; M84739; AAA51916.1; -

EMBL; M32294; AAA36582.1; -

EMBL; AD000092; AAB51176.1; -

PIR; A37047; A37047.

PIR; S11475; S11475.

PIR; A42330; A42330.

PIR; A46452; A46452.

SWISS-2DPAGE; P27797; HUMAN.

Aarhus/Ghent-2DPAGE; 9401; IEF.

HSC-2DPAGE; P27797; HUMAN.

MIM: 109091; -

InterPro; IPR001580; Calreticulin.

InterPro; IPR000886; ER-target.

Pfam; PF00262; calreticulin; 1.

PRINTS; PR00626; CALRETICULIN.

ProDom; PD001866; Calreticulin; 1.

PROSITE; PS00014; ER-TARGET; 1.

PROSITE; PS00803; CALRETICULIN; 1.

PROSITE; PS00804; CALRETICULIN; 2; 1.

PROSITE; PS00805; CALRETICULIN-REPEAT; 3.

KW Endoplasmic reticulum; Calcium-binding; Repeat; Signal.

SIGNAL 1 17

CHAIN 18 417

DOMAIN 18 197

DOMAIN 198 308

DOMAIN 309 417

DOMAIN 191 255

REPEAT 191 202

1-1.

FT REPEAT 210 221 1-2.  
 FT REPEAT 227 238 1-3.  
 FT REPEAT 244 255 1-4.  
 FT DOMAIN 259 297 3 X APPROXIMATE REPEATS.  
 FT REPEAT 259 269 2-1.  
 FT REPEAT 273 283 2-2.  
 FT REPEAT 287 297 2-3.  
 FT DOMAIN 351 408 ASP/GLU/LYS-RICH.  
 FT DISULFID 137 163 BY SIMILARITY.  
 FT SITE 414 417 PREVENT SECRETION FROM ER.  
 FT CONFLICT 35 35 MISSING (IN REF. 3).  
 SQ SEQUENCE 417 AA; 48141 MW; BC37C3C0F1054FB2 CRC64;

Query Match 100.0%; Score 96; DB 1; Length 417;  
 Best Local Similarity 100.0%; Pred. NO. 1.4e-07;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VIFNYKGNVLINKDIRC 18

Db 146 VIFNYKGNVLINKDIRC 163

RESULT 5

CRTC\_RABIT

ID CRTC\_RABIT STANDARD; PRT; 418 AA.

AC P15253;

DT 01-APR-1990 (Rel. 14, Created)

DT 01-APR-1990 (Rel. 14, Last sequence update)

DT 01-OCT-1996 (Rel. 34, Last annotation update)

DE CALRETICULIN PRECURSOR (CRP55) (CALREUCULIN) (HACBP) (ERP60).

GN CALR.

OS Oryctolagus cuniculus (Rabbit).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.

OX NCBI\_TaxID:9986;

RN [1]

RP SEQUENCE FROM N.A.

TISSUE-Slow-twitch skeletal muscle;

RC MEDLINE-90094320; PubMed-2600080;

RA Fliegel L., Burns K., MacLennan D.H., Reithmeier R.A.F., Michalak M.;

\*Molecular cloning of the high affinity calcium-binding protein

(calreticulin) of skeletal muscle sarcoplasmic reticulum.";

RL J. Biol. Chem. 264:21522-21528(1989).

RN [2]

RP SEQUENCE FROM N.A.

TISSUE-Fast-twitch skeletal muscle;

RC MEDLINE-91282795; PubMed-2059224;

RA Fliegel L., Michalak M.;

\*Fast-twitch and slow-twitch skeletal muscles express the same

isoform of calreticulin.";

RL Biochem. Biophys. Res. Commun. 177:979-984(1991).

RN [3]

RP SEQUENCE OF 18-36.

RC MEDLINE-91054414; PubMed-2241926;

RA Treves S., de Mattei M., Lanfredi M., Villa A., Green N.M.,

MacLennan D.H., Meldolesi J., Pozzan T.;

\*Calreticulin is a candidate for a calsequestrin-like function in

Ca2(+)-storage compartments (calciosomes) of liver and brain.";

RL Biochem. J. 271:473-480(1990).

RN [4]

RP SEQUENCE OF 18-46.

RC MEDLINE-91201375; PubMed-2016321;

RA Milner R.E., Baksh S., Shemanko C., Carpenter M.R., Smillie L.,

Vance J.E., Opas M., Michalak M.;

\*Calreticulin, and not calsequestrin, is the major calcium binding

protein of smooth muscle sarcoplasmic reticulum and liver endoplasmic

reticulum.";

RL J. Biol. Chem. 266:7155-7165(1991).

RN [5]

RP PARTIAL SEQUENCE.

RC TISSUE-Lung;

RE MEDLINE-92002038; PubMed-1911780;



RA Guan S., Fallick A.M., Williams D.E., Cashman J.R.;  
 RT "Evidence for complex formation between rabbit lung flavin-containing  
 RL monooxygenase and calreticulin.";  
 CC Biochemistry 30:9892-9900(1991).  
 CC -!- FUNCTION: THIS PROTEIN BINDS CALCIUM. THERE ARE BOTH HIGH AND  
 CC LOW AFFINITY CALCIUM-BINDING SITES.  
 CC -!- SUBUNIT: MONOMER (BY SIMILARITY).  
 CC -!- SUBCELLULAR LOCATION: ENDOPLASMIC RETICULUM LUMEN.  
 CC -!- SIMILARITY: BELONGS TO THE CALRETICULIN FAMILY.  
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 CC -----  
 DR EMBL; J05138; AAA31188.1; -;  
 DR PIR; A34154; A34154.  
 DR PIR; C33208; C33208.  
 DR PIR; D33208; D33208.  
 DR PIR; E33208; E33208.  
 DR PIR; F33208; F33208.  
 DR PIR; S13046; S13046.  
 DR PIR; S13047; S13047.  
 DR InterPro; IPR001580; Calreticulin.  
 DR InterPro; IPR000886; ER target.  
 DR Pfam; PF00262; Calreticulin; 1.  
 DR PRINTS; PR00626; CALRETICULIN.  
 DR PRODOM; PD001866; Calreticulin; 1.  
 DR PROSITE; PS00014; ER\_TARGET; 1.  
 DR PROSITE; PS00803; CALRETICULIN\_1; 1.  
 DR PROSITE; PS00804; CALRETICULIN\_2; 1.  
 DR PROSITE; PS00805; CALRETICULIN\_REPEAT; 3.  
 KW Endoplasmic reticulum; Calcium-binding; Repeat; Signal.  
 FT SIGNAL 1 17  
 FT CHAIN 18 418 CALRETICULIN.  
 FT DOMAIN 18 197 N-DOMAIN.  
 FT DOMAIN 198 308 P-DOMAIN.  
 FT DOMAIN 309 418 C-DOMAIN.  
 FT DOMAIN 191 -255 4 X APPROXIMATE REPEATS.  
 FT REPEAT 191 202 1-1.  
 FT REPEAT 210 221 1-2.  
 FT REPEAT 227 238 1-3.  
 FT REPEAT 244 255 1-4.  
 FT DOMAIN 259 297 3 X APPROXIMATE REPEATS.  
 FT REPEAT 259 269 2-1.  
 FT REPEAT 273 283 2-2.  
 FT REPEAT 287 297 2-3.  
 FT DOMAIN 351 408 ASP/GLU/LYS-RICH.  
 FT DISULFID 137 163 BY SIMILARITY.  
 FT SITE 415 418 PREVENT SECRETION FROM ER.  
 FT VARIANT 35 35 E->D.  
 FT CONFLICT 90 90 P -> T (IN REF. 5).  
 SQ SEQUENCE 418 AA; 48275 MW; B6082B689DC763A6 CRC64;

Query Match 100.0%; Score 96; DB 1; Length 418;  
 Best Local Similarity 100.0%; Pred. No. 1.4e-07;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VIFNYKGNVLINKDIRC 18  
 |||||  
 Db 146 VIFNYKGNVLINKDIRC 163  
 |||||

RESULT 6  
 ID CRT2\_BOVIN STANDARD; PRT; 421 AA.  
 AC P42918;  
 DT 01-NOV-1995 (Rel. 32, Created)  
 DT 01-NOV-1995 (Rel. 32, Last sequence update)

DT 15-JUL-1998 (Rel. 36, Last annotation update)  
 DE CALRETICULIN, BRAIN ISOFORM 2 PRECURSOR (CRP55) (CALREGULIN) (HACBP).  
 OS Bos taurus (Bovine).  
 CC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
 CC Bovidae; Bovinae; Bos.  
 CC NCBI\_TaxID=9913;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Brain;  
 RX MEDLINE=93385184; PubMed=8373827;  
 RA Liu N., Fine R.E., Johnson R.J.;  
 RT "Comparison of cDNAs from bovine brain coding for two isoforms of  
 RT calreticulin.";  
 RL Biochim. Biophys. Acta 1202:70-76(1993).  
 CC -!- FUNCTION: THIS PROTEIN BINDS CALCIUM. THERE ARE BOTH HIGH AND  
 CC LOW AFFINITY CALCIUM-BINDING SITES.  
 CC -!- SUBUNIT: MONOMER (BY SIMILARITY).  
 CC -!- SUBCELLULAR LOCATION: ENDOPLASMIC RETICULUM LUMEN.  
 CC -!- SIMILARITY: BELONGS TO THE CALRETICULIN FAMILY.  
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 CC -----  
 DR EMBL; L13462; AAC37307.1; -;  
 DR InterPro; IPR001580; Calreticulin.  
 DR InterPro; IPR000886; ER target.  
 DR Pfam; PF00262; calreticulin; 1.  
 DR PRINTS; PR00626; CALRETICULIN.  
 DR PRODOM; PD001866; Calreticulin; 1.  
 DR PROSITE; PS00014; ER\_TARGET; 1.  
 DR PROSITE; PS00803; CALRETICULIN\_1; 1.  
 DR PROSITE; PS00804; CALRETICULIN\_2; 1.  
 DR PROSITE; PS00805; CALRETICULIN\_REPEAT; 3.  
 KW Endoplasmic reticulum; Calcium-binding; Repeat; Signal.  
 FT SIGNAL 1 34 POTENTIAL.  
 FT CHAIN 35 421 CALRETICULIN, BRAIN ISOFORM 2.  
 FT DOMAIN 35 201 N-DOMAIN.  
 FT DOMAIN 202 312 P-DOMAIN.  
 FT DOMAIN 313 421 C-DOMAIN.  
 FT DOMAIN 195 259 4 X APPROXIMATE REPEATS.  
 FT REPEAT 195 206 1-1.  
 FT REPEAT 214 225 1-2.  
 FT REPEAT 231 242 1-3.  
 FT REPEAT 248 259 1-4.  
 FT DOMAIN 263 301 3 X APPROXIMATE REPEATS.  
 FT REPEAT 263 273 2-1.  
 FT REPEAT 277 287 2-2.  
 FT REPEAT 291 301 2-3.  
 FT DOMAIN 366 411 ASP/GLU/LYS-RICH.  
 FT DISULFID 141 167 BY SIMILARITY.  
 FT CARBOHYD 183 183 N-LINKED (GLCNAC. .) (POTENTIAL).  
 FT SITE 418 421 PREVENT SECRETION FROM ER.  
 SQ SEQUENCE 421 AA; 48812 MW; 0257E959F71528BC CRC64;

Query Match 100.0%; Score 96; DB 1; Length 421;  
 Best Local Similarity 100.0%; Pred. No. 1.4e-07;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VIFNYKGNVLINKDIRC 18  
 |||||  
 Db 150 VIFNYKGNVLINKDIRC 167  
 |||||

RESULT 7  
 ID CRTC\_DROME STANDARD; PRT; 406 AA.

P29413; Q9VHA3;  
 01-APR-1993 (Rel. 25, Created)  
 01-OCT-1993 (Rel. 27, Last sequence update)  
 20-AUG-2001 (Rel. 40, Last annotation update)  
 DE CALRETICULIN PRECURSOR (CRP55) (CALRETCULIN) (HACBP).  
 CAC OR CG9429.  
 GN Drosophila melanogaster (Fruit fly).  
 OS Eukaryota; Metazoa; Arthropoda; Insecta;  
 OC Prexygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
 OX Ephyroidae; Drosophilidae; Drosophila.  
 NCBI\_TaxID: 7227;  
 [1]  
 SEQUENCE FROM N.A.  
 RX MEDLINE 93208374; PubMed 1296819;  
 NA Smith M.J.;  
 RT "Nucleotide sequence of a Drosophila melanogaster gene encoding a  
 calreticulin homologue";  
 RL DNA Seq. 3:247-250(1992).  
 [2]  
 SEQUENCE FROM N.A.  
 RC STRAIN BERKELEY;  
 RX MEDLINE 20196006; PubMed 10731132;  
 RA Adams M.D., Colnider S.E., Holt R.A., Evans C.A., Gocayne J.D.,  
 RA Anagnostides P.G., Scher S.E., Li P.W., Hoskins R.A., Galle R.F.,  
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,  
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,  
 RA Brannon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,  
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,  
 RA Abell J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,  
 RA Ballwe R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,  
 RA Benson K.Y., Bencos P.V., Beriman B.P., Bhandari D., Bolshakov S.,  
 RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotter P.,  
 RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,  
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,  
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,  
 RA Dodson K., Doup L.E., Downs M., Dugan-Rocha S., Dunkov B.C., Dunn P.,  
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,  
 RA Foeller C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,  
 RA Glodok A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,  
 RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,  
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam J.,  
 RA Jalili M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,  
 RA Kimmel B.E., Kodira C., Kraft C., Kravitz S., Kulp D., Lai Z.,  
 RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,  
 RA Liu X., Mattel B., McIntosh T.C., McLeod M.P., McPherson D.,  
 RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,  
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,  
 RA Nelson D.M., Nelson K.A., Nixon K., Nusskern D.R., Pacle J.M.,  
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,  
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,  
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,  
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,  
 RA Sivakus R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,  
 RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissbach J.,  
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,  
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,  
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,  
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;  
 RT "The genome sequence of Drosophila melanogaster";  
 RL Science 287:2185-2195(2000).  
 [3]  
 SEQUENCE OF 91-124 AND 182-220.  
 RX MEDLINE 90307981; PubMed 2365822;  
 NA McCaulliffe D.P., Zappi E., Lieu T.S., Michalak M., Sontheimer R.D.,  
 RA Capra J.D.;  
 RT "A human Ro/SS-A autoantigen is the homologue of calreticulin and is  
 highly homologous with onchocercal RAL-1 antigen and an alysia  
 'memory molecule'";  
 RL J. Clin. Invest. 86:332-335(1990).  
 CC -!- FUNCTION: THIS PROTEIN BINDS CALCIUM. THERE ARE BOTH HIGH AND  
 LOW AFFINITY CALCIUM-BINDING SITES.  
 CC -!- SUBCELLULAR LOCATION: ENDOPLASMIC RETICULUM LUMEN.  
 CC -!- SIMILARITY: BELONGS TO THE CALRETICULIN FAMILY.

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 CC -----  
 DR EMBL; X64461; CAA45791.1; -.  
 DR EMBL; AE003683; AAF54416.1; -.  
 DR PIR; A37158; A37158.  
 DR FlyBase; FBgn0005585; Crc.  
 DR InterPro; IPR001580; Calreticulin.  
 DR InterPro; IPR000886; ER\_target.  
 DR Pfam; PF00262; calreticulin; 1.  
 DR PRINTS; PR00626; CALRETICULIN.  
 DR PRODOM; PD001866; Calreticulin; 1.  
 DR PROSITE; PS00014; ER\_TARGET; 1.  
 DR PROSITE; PS00803; CALRETICULIN\_1; 1.  
 DR PROSITE; PS00804; CALRETICULIN\_2; 1.  
 DR PROSITE; PS00805; CALRETICULIN\_REPEAT; 3.  
 KW Endoplasmic reticulum; Calcium-binding; Repeat; Signal.  
 FT SIGNAL 1 17 POTENTIAL.  
 FT CHAIN 18 406 CALRETICULIN.  
 FT CONFLICT 107 107 G -> A (IN REF. 3).  
 FT CONFLICT 184 184 V -> L (IN REF. 3).  
 SQ SEQUENCE 406 AA; 46808 MW; 65D72C69D0BEC427 CRC64;  
 Query Match 82.3%; Score 79; DB 1; Length 406;  
 Best Local Similarity 83.3%; Pred. No. 5.6e-05;  
 Matches 15; Conservative 2; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 VIFNYKGNVLINKDIRC 18  
 DB 146 VIFSYKGNHLISKDIRC 163  
 III:IIII III:IIII  
 RESULT 8  
 CRTCSCHMA  
 ID CRTCSCHMA STANDARD; PRT; 393 AA.  
 AC Q06814; Q26562;  
 DT 01-JUN-1994 (Rel. 29, Created)  
 DT 01-FEB-1996 (Rel. 33, Last sequence update)  
 DT 01-NOV-1997 (Rel. 35, Last annotation update)  
 DE CALRETICULIN PRECURSOR (SM4 PROTEIN).  
 OS Schistosoma mansoni (Blood fluke).  
 OC Eukaryota; Metazoa; Platyhelminthes; Turbellarian Platyhelminths;  
 OC Rhabdiorhiza; Eulcithophora; Platyhelminthes; Digenea; Strigoida; Schistosomatoidea;  
 OC Neodermata; Trematoda; Reversospermatia; Mediofusata;  
 OC Schistosomatidae; Schistosoma.  
 OX NCBI\_TaxID-6183;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-PUERTO RICAN;  
 RX MEDLINE-93165070; PubMed-8433712;  
 RA Khalife J., Trottein F., Schacht A.-M., Godin C., Pierce R.J.,  
 RA Capron A.;  
 RT "Cloning of the gene encoding a Schistosoma mansoni antigen  
 homologous to human Ro/SS-A autoantigen";  
 RL Mol. Biochem. Parasitol. 57:193-202(1993).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-PUERTO RICAN;  
 RX MEDLINE-94187805; PubMed-8139623;  
 RA Khalife J., Pierce R.J., Godin C., Capron A.;  
 RT "Cloning and sequencing of the gene encoding Schistosoma mansoni  
 calreticulin";  
 RL Mol. Biochem. Parasitol. 62:313-315(1993).  
 CC -!- FUNCTION: THIS PROTEIN BINDS CALCIUM. THERE ARE BOTH HIGH AND  
 CC LOW AFFINITY CALCIUM-BINDING SITES.  
 CC -!- SUBCELLULAR LOCATION: ENDOPLASMIC RETICULUM LUMEN.

CC -!- SIMILARITY: BELONGS TO THE CALRETICULIN FAMILY.  
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CC -----  
DR EMBL: M93097; AAA29854.1; -;  
DR EMBL: L24159; AAA19024.1; -;  
DR HSP: P00268; 4RXN.  
DR InterPro: IPR001580; Calreticulin.  
DR Pfam: PF00262; calreticulin; 1.  
DR PRINTS: PR00626; CALRETICULIN.  
DR PROSITE: PS00803; Calreticulin; 1.  
DR PROSITE: PS00804; CALRETICULIN\_2; 1.  
DR PROSITE: PS00805; CALRETICULIN\_REPEAT; 1.  
KW Endoplasmic reticulum; Calcium-binding; Repeat; Signal; Glycoprotein.  
FT SIGNAL 1 16 POTENTIAL.  
FT CHAIN 17 393 CALRETICULIN.  
FT DOMAIN 189 254 4 X 12 AA APPROXIMATE REPEATS.  
FT REPEAT 189 200 1-1.  
FT REPEAT 209 220 1-2.  
FT REPEAT 225 236 1-3.  
FT REPEAT 243 254 1-4.  
FT DOMAIN 257 295 3 X 11 AA APPROXIMATE REPEATS.  
FT REPEAT 257 267 2-1.  
FT REPEAT 271 281 2-2.  
FT REPEAT 285 295 2-3.  
FT CARBOHYD 27 27 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT DISULFID 135 161 BY SIMILARITY.  
FT SITE 390 393 PREVENT SECRETION FROM ER.  
FT CONFLICT 89 90 MV -> IL (IN REF. 2).  
FT CONFLICT 188 207 MISSING (IN REF. 2).  
FT CONFLICT 378 378 Y -> D (IN REF. 2).  
SQ SEQUENCE 393 AA; 45397 MW; 45F59857C21940D2 CRC64;

Query Match 75.0%; Score 72; DB 1; Length 393;  
Best Local Similarity 77.8%; Pred. No. 0.00065;  
Matches 14; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 VIFNYKGNVLINKDIRC 18  
|||:|||||:|:|:|  
DB 144 VIFNYKGNHLIKKEIPC 161

RESULT 9  
RALL\_ONCVO STANDARD; PRT; 388 AA.  
AC P11012;  
DT 01-JUL-1989 (Rel. 11, Created)  
DT 01-NOV-1995 (Rel. 32, Last sequence update)  
DT 01-OCT-1996 (Rel. 34, Last annotation update)  
DE RAL-1 PROTEIN PRECURSOR (41 KDA LARVAL ANTIGEN).  
GN RAL1.  
OS Onchocerca volvulus.  
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Spirurida; Filarioidea;  
OX Onchocercidae; Onchocerca.  
OX NCBI\_TaxID=6282;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=94341871; PubMed=7520419;  
RA Rokeach L.A., Zimmerman P.A., Unnasch T.R.;  
RT "Epitopes of the Onchocerca volvulus RAL1 antigen, a member of the  
RT calreticulin family of proteins, recognized by sera from patients  
RT with onchocerciasis."  
RL Infect. Immun. 62:3696-3704(1994).

RN SEQUENCE OF 53-388 FROM N.A.  
RX MEDLINE=88273584; PubMed=2455736;  
RA Unnasch T.R., Gallin M.Y., Soboslay P.T., Ertmann K.D., Greene B.M.;  
RT "Isolation and characterization of expression cDNA clones encoding  
RT antigens of Onchocerca volvulus infective larvae."  
RL J. Clin. Invest. 82:262-269(1988).  
CC -!- SIMILARITY: BELONGS TO THE CALRETICULIN FAMILY.  
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CC -----  
DR EMBL: M20565; AAA59056.1; -;  
DR PIR: A32507; A32507.  
DR InterPro: IPR001580; Calreticulin.  
DR Pfam: PF00262; calreticulin; 1.  
DR PRINTS: PR00626; CALRETICULIN.  
DR PRODOM: PD001866; Calreticulin; 1.  
DR PROSITE: PS00803; Calreticulin; 1.  
DR PROSITE: PS00804; CALRETICULIN\_2; 1.  
DR PROSITE: PS00805; CALRETICULIN\_REPEAT; 3.  
KW Calcium-binding; Repeat; Antigen; Signal.  
FT SIGNAL 1 17 POTENTIAL.  
FT CHAIN 18 388 RAL-1 PROTEIN.  
FT DOMAIN 189 253 4 X APPROXIMATE REPEATS.  
FT REPEAT 189 200 1-1.  
FT REPEAT 208 219 1-2.  
FT REPEAT 225 236 1-3.  
FT REPEAT 242 253 1-4.  
FT DOMAIN 257 295 3 X APPROXIMATE REPEATS.  
FT REPEAT 257 267 2-1.  
FT REPEAT 271 281 2-2.  
FT REPEAT 285 295 2-3.  
FT DOMAIN 353 388 ARG/LYS-RICH (BASIC).  
FT DISULFID 135 161 BY SIMILARITY.  
SQ SEQUENCE 388 AA; 45298 MW; 9537F298A2D31CD6 CRC64;

Query Match 68.8%; Score 66; DB 1; Length 388;  
Best Local Similarity 66.7%; Pred. No. 0.0054;  
Matches 12; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 VIFNYKGNVLINKDIRC 18  
|||:|||||:|:|:|  
DB 144 VIFHYKDRNHMTKKDIRC 161

RESULT 10  
CRIC\_CAEEL STANDARD; PRT; 395 AA.  
AC P27798;  
DT 01-AUG-1992 (Rel. 23, Created)  
DT 01-AUG-1992 (Rel. 23, Last sequence update)  
DT 01-FEB-1994 (Rel. 28, Last annotation update)  
DE CALRETICULIN PRECURSOR.  
GN CRT-1.  
OS Caenorhabditis elegans.  
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;  
OX Rhabditidae; Peloderinae; Caenorhabditis.  
OX NCBI\_TaxID=6239;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN-BRISTOL N2;  
RX MEDLINE=92329978; PubMed=1627827;  
RA Smith M.J.;  
RT "A C. elegans gene encodes a protein homologous to mammalian  
RT calreticulin."  
RL DNA Seq. 2:235-240(1992).



DR PRINTS; PR00626; CALRETICULIN.  
 DR PRODM; PD001866; Calreticulin; 1.  
 DR PROSITE; PS00804; CALRETICULIN\_2; 1.  
 DR PROSITE; PS00805; CALRETICULIN\_REPEAT; 1.  
 DR PROSITE; PS00014; ER\_TARGET; 1.  
 KW Endoplasmic reticulum; Calcium-binding; Repeat; Signal.  
 FT SIGNAL 1 19 POTENTIAL.  
 FT CHAIN 20 424 CALRETICULIN.  
 FT DOMAIN 191 257 4 X 12 AA APPROXIMATE REPEATS.  
 FT REPEAT 191 202 1-1.  
 FT REPEAT 211 222 1-2.  
 FT REPEAT 227 238 1-3.  
 FT REPEAT 246 257 1-4.  
 FT REPEAT 260 298 3 X 11 AA APPROXIMATE REPEATS.  
 FT REPEAT 260 270 2-1.  
 FT REPEAT 274 284 2-2.  
 FT REPEAT 288 298 2-3.  
 FT DISULFID 105 137 BY SIMILARITY.  
 FT SITE 421 424 PREVENT SECRETION FROM ER (POTENTIAL).  
 SQ SEQUENCE 424 AA; 48350 MW; BAF273694FB6FC37 CRC64;

Query Match 61.5%; Score 59; DB 1; Length 424;  
 Best Local Similarity 75.0%; Pred. No. 0.07;  
 Matches 12; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 1 VIFNYKGNVLINKDI 16  
 || ||||| || ||  
 DB 145 VILNYKGNHLKKEI 160

RESULT 13  
 CRTC\_EUGGR STANDARD; PRT; 401 AA.  
 AC Q92NY3;  
 DT 20-AUG-2001 (Rel. 40, Created)  
 DT 20-AUG-2001 (Rel. 40, Last sequence update)  
 DT 20-AUG-2001 (Rel. 40, Last annotation update)  
 DE CALRETICULIN PRECURSOR.  
 OS Euglena gracilis.  
 OC Eukaryota; Euglenozoa; Euglenida; Euglenales; Euglena.  
 OX NCBI\_TaxID=3039;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Navazzo L., Baldan B., Martin W., Mariani P.;  
 RT "Evidence for conservation of a calcium homeostat component:  
 purification characterization and cloning of calreticulin from Euglena  
 gracilis.";  
 RL Submitted (DEC-1996) to the EMBL/GenBank/DBJ databases.  
 CC -!- FUNCTION: THIS PROTEIN BINDS CALCIUM. THERE ARE BOTH HIGH AND  
 CC LOW AFFINITY CALCIUM-BINDING SITES (BY SIMILARITY).  
 CC -!- SUBCELLULAR LOCATION: ENDOPLASMIC RETICULUM LUMEN (BY SIMILARITY).  
 CC -!- SIMILARITY: BELONGS TO THE CALRETICULIN FAMILY.  
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 DR EMBL; Y09816; CAA70945.1; -  
 DR InterPro; IPR001580; Calreticulin.  
 DR InterPro; IPR000886; ER\_target.  
 DR Pfam; PF00262; calreticulin; 1.  
 DR PRINTS; PR00626; CALRETICULIN.  
 DR PRODM; PD001866; Calreticulin; 1.  
 DR PROSITE; PS00014; ER\_TARGET; 1.  
 DR PROSITE; PS00803; CALRETICULIN\_1; 1.  
 DR PROSITE; PS00804; CALRETICULIN\_2; 1.  
 DR PROSITE; PS00805; CALRETICULIN\_REPEAT; 2.  
 KW Endoplasmic reticulum; Calcium-binding; Repeat; Signal; Glycoprotein.  
 FT SIGNAL 1 25 POTENTIAL.  
 FT CHAIN 26 416 CALRETICULIN.  
 FT CARBOHYD 157 157 N-LINKED (GLCNAC. .) (POTENTIAL).  
 FT CARBOHYD 57 57 N-LINKED (GLCNAC. .) (POTENTIAL).  
 FT SITE 413 416 PREVENT SECRETION FROM ER (POTENTIAL).  
 SQ SEQUENCE 416 AA; 48136 MW; 565FEC3489F77CA7 CRC64;

Query Match 55.2%; Score 53; DB 1; Length 416;  
 Best Local Similarity 58.8%; Pred. No. 0.58;  
 Matches 10; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

OY 2 IFNYKGNVLINKDIRC 18  
 ||||| || || ||  
 DB 143 ILTYKGNLLWKKEPC 159

RESULT 14  
 CRTC\_BETVU STANDARD; PRT; 416 AA.  
 AC O81919;  
 DT 20-AUG-2001 (Rel. 40, Created)  
 DT 20-AUG-2001 (Rel. 40, Last sequence update)  
 DT 20-AUG-2001 (Rel. 40, Last annotation update)  
 DE CALRETICULIN PRECURSOR.  
 OS Beta vulgaris (Sugar beet).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 OC Caryophyllales; Caryophyllales; Chenopodiaceae; Beta.  
 OX NCBI\_TaxID=3555;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-VV-D/ZR5; TISSUE=Leaf;  
 RA Viereck R.;  
 RT "Nucleotide sequence from sugar beet calreticulin.";  
 RL Submitted (OCT-1997) to the EMBL/GenBank/DBJ databases.  
 CC -!- FUNCTION: THIS PROTEIN BINDS CALCIUM. THERE ARE BOTH HIGH AND  
 CC LOW AFFINITY CALCIUM-BINDING SITES (BY SIMILARITY).  
 CC -!- SUBCELLULAR LOCATION: ENDOPLASMIC RETICULUM LUMEN (BY SIMILARITY).  
 CC -!- SIMILARITY: BELONGS TO THE CALRETICULIN FAMILY.  
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 DR EMBL; AJ002057; CAA05161.1; -  
 DR Mendel; J32549; Betvu; J166; J32549.  
 DR InterPro; IPR001580; Calreticulin.  
 DR InterPro; IPR000886; ER\_target.  
 DR Pfam; PF00262; calreticulin; 1.  
 DR PRINTS; PR00626; CALRETICULIN.  
 DR PRODM; PD001866; Calreticulin; 1.  
 DR PROSITE; PS00014; ER\_TARGET; 1.  
 DR PROSITE; PS00803; CALRETICULIN\_1; 1.  
 DR PROSITE; PS00804; CALRETICULIN\_2; 1.  
 DR PROSITE; PS00805; CALRETICULIN\_REPEAT; 2.  
 KW Endoplasmic reticulum; Calcium-binding; Repeat; Signal; Glycoprotein.  
 FT SIGNAL 1 25 POTENTIAL.  
 FT CHAIN 26 416 CALRETICULIN.  
 FT CARBOHYD 157 157 N-LINKED (GLCNAC. .) (POTENTIAL).  
 FT CARBOHYD 57 57 N-LINKED (GLCNAC. .) (POTENTIAL).  
 FT SITE 413 416 PREVENT SECRETION FROM ER (POTENTIAL).  
 SQ SEQUENCE 416 AA; 48136 MW; 565FEC3489F77CA7 CRC64;

Db 153 IFNYNDTNHLIKKDVPC 169

## RESULT 15

```
CRT3_ARATH
ID CRT3_ARATH STANDARD; PRT; 424 AA.
AC 004153; Q98JE7;
DT 20-AUG-2001 (Rel. 40, Created)
DT 20-AUG-2001 (Rel. 40, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE CALRETICULIN 3 PRECURSOR.
GN CRT3 OR T27G7.13.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID:3702;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE 97303616; PubMed-9159940;
RA Nelson D.E., Glaunsinger B., Bohnert H.J.;
RT *Abundant accumulation of the calcium-binding molecular chaperone
RT calreticulin in specific floral tissues of Arabidopsis thaliana.*;
RL Plant Physiol. 114:29-37(1997).
RN [2]
RP SEQUENCE FROM N.A.
RA Shinn P., Brooks S., Buehler E., Chao Q., Johnson-Hopson C., Khan S.,
RA Kim C., Altafi H., Bel Q., Chin C., Chiou J., Chol E., Conn L.,
RA Conway A., Gonzales A., Hansen N., Howing B., Koo T., Lam B., Lee J.,
RA Lenz C., Li J., Liu A., Liu K., Liu S., Mukharasy N., Nguyen M.,
RA Palm C., Pham P., Sakano H., Schwartz J., Southwick A., Thaveri A.,
RA Toriumi M., Vaysberg M., Yu G., Federspiel N.A., Theologis A.,
RA Ecker J.R.;
RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: THIS PROTEIN BINDS CALCIUM. THERE ARE BOTH HIGH AND
CC -!- LOW AFFINITY CALCIUM-BINDING SITES (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: ENDOPLASMIC RETICULUM LUMEN (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE CALRETICULIN FAMILY.
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CC -----
DR EMBL; U66345; AAC49697.1; -.
DR EMBL; AC006932; AAF22902.1; ALT_SEQ.
DR Mende; 16507; Arath;1166;16507.
DR InterPro; IPR001580; Calreticulin.
DR InterPro; IPR000886; ER_target.
DR Pfam; PF00262; calreticulin; 1.
DR PRINTS; PR00626; CALRETICULIN.
DR PRODOM; PD001866; Calreticulin; 1.
DR PROSITE; PS00014; ER_TARGET; 1.
DR PROSITE; PS00803; CALRETICULIN_1; 1.
DR PROSITE; PS00804; CALRETICULIN_2; 1.
DR PROSITE; PS00805; CALRETICULIN_REPEAT; FALSE_NEG.
DR Endoplasmic reticulum; Calcium-binding; Repeat; Signal; Glycoprotein;
KW Multigene family.
FT SIGNAL 1 28 POTENTIAL.
FT CHAIN 29 424 CALRETICULIN 3
FT CARBOHYD 97 97 N-LINKED (GLCNAC. .) (POTENTIAL).
FT SITE 421 424 PREVENT SECRETION FROM ER (POTENTIAL).
FT CONFLICT 279 279 F -> S (IN REF. 2).
SQ SEQUENCE 424 AA; 49904 MW; 650E0AE8342F0B97 CRC64;
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Query Match 54.2%; Score 52; DB 1; Length 424;  
Best Local Similarity 50.0%; Pred. No. 0.84; Indels 0; Gaps 0;  
Matches 9; Conservative 5; Mismatches 4;

QY 1 VIFNYKGNVLINKDIRC 18  
|| :||:| | ||:  
Db 155 VIVSYGGQNYPIKKDLQC 172

Search completed: January 9, 2002, 15:12:15  
Job time: 657 sec

GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: January 9, 2002, 15:02:03 ; Search time 43.73 Seconds  
(without alignments)  
31.355 Million cell updates/sec

Title: US-09-828-000-6

Perfect score: 96  
Sequence: 1 VIFNYGKNVLINKDIRC 18

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues

Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR\_68: \*  
1: pir1: \*  
2: pir2: \*  
3: pir3: \*  
4: pir4: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	96	100.0	400	2 S43376	calreticulin, brai
2	96	100.0	416	1 S06763	calreticulin, precu
3	96	100.0	416	2 JH0819	calreticulin, precu
4	96	100.0	417	1 A37047	calreticulin, precu
5	96	100.0	418	1 A34154	calreticulin, precu
6	96	100.0	421	2 S36799	calreticulin, precu
7	86	89.6	405	1 JH0795	calreticulin, precu
8	79	82.3	406	2 A56637	calreticulin, homol
9	78	81.2	419	2 S71343	calreticulin, precu
10	73	76.0	384	2 S29130	calreticulin (clon
11	73	76.0	411	2 S29129	calreticulin, precu
12	72	75.0	393	1 A48573	calreticulin, autoa
13	66	68.8	336	2 A32507	41K larval antigen
14	64	66.7	395	2 S25851	calreticulin, precu
15	53	55.2	416	2 T14554	calreticulin - bee
16	51	53.1	725	1 IJMSNG	neural cell adhesi
17	51	53.1	761	1 IJHUNG	neural cell adhesi
18	51	53.1	853	1 IJBONC	neural cell adhesi
19	51	53.1	858	1 IJRTNC	neural cell adhesi
20	51	53.1	1091	1 IJCHNL	neural cell adhesi
21	51	53.1	1115	1 IJMSNL	neural cell adhesi
22	48	50.0	464	2 A53101	vitamin D3 hydroxy
23	47	49.0	725	2 JE0099	neural cell adhesi
24	47	49.0	725	2 JE0100	neural cell adhesi
25	47	49.0	1088	1 IJXLNL	neural cell adhesi
26	47	49.0	1092	1 JN0635	neural cell adhesi
27	45	46.9	412	2 T05703	calreticulin - bar
28	45	46.9	415	2 T05705	calreticulin - bar
29	45	46.9	501	2 T44939	glyceraldehyde-3-p

30	44	45.8	417	2 A64380	phosphoglycerate k
31	44	45.8	421	2 S58170	calreticulin, precu
32	44	45.8	425	2 C96605	calreticulin (Crt1
33	44	45.8	496	2 S33597	protein kinase chk
34	43	44.8	103	2 G71141	hypothetical prote
35	43	44.8	247	2 PC4260	activin type I rec
36	43	44.8	257	2 C75077	iron (iii) abc tra
37	43	44.8	327	2 B82918	DNA-directed RNA p
38	43	44.8	415	2 T10172	calreticulin - cas
39	43	44.8	435	2 S23580	probable protein k
40	43	44.8	767	2 B84594	probable LRR recep
41	42	43.8	103	2 F75010	hypothetical prote
42	42	43.8	121	2 B56272	probable pheromone
43	42	43.8	154	2 A60998	replication protei
44	42	43.8	222	2 H71260	probable glucose-1
45	42	43.8	284	2 T49025	carbonate dehydrat

ALIGNMENTS

RESULT 1  
S43376  
calreticulin, brain isoform 1 - bovine  
C:Species: Bos primigenius taurus (cattle)  
C:Date: 20-Oct-1994 #sequence\_revision 23-Mar-1995 #text\_change 07-May-1999  
C:Accession: S43376; S36801  
R:Matsuoka, K.; Seta, K.; Yamakawa, Y.; Okuyama, T.; Shinoda, T.; Isobe, T.  
Biochem. J. 298, 435-442, 1994  
A:Title: Covalent structure of bovine brain calreticulin.  
A:Reference number: S43376; MUID:94183174  
A:Accession: S43376  
A:Molecule type: protein  
A:Residues: 1-400 <MAT>  
A:Experimental source: brain  
R:Liu, N.; Fine, R.E.; Johnson, R.J.  
Biochim. Biophys. Acta 1202, 70-76, 1993  
A:Title: Comparison of cDNAs from bovine brain coding for two isoforms of calreticuli  
A:Reference number: S36799; MUID:93385184  
A:Accession: S36801  
A>Status: nucleic acid sequence not shown  
A:Molecule type: mRNA  
A:Residues: 45-63, 'E', 65-83 <LIU>  
A:Experimental source: brain, clone 8.1  
C:Superfamily: calreticulin  
C:Keywords: calcium binding; glycoprotein  
F:397-400/Region: endoplasmic reticulum retention signal  
F:120-146/Disulfide bonds: #status experimental  
F:162/Binding site: carbohydrate (Asn) (covalent) #status experimental

Query Match 100.0%; Score 96; DB 2; Length 400;  
Best Local Similarity 100.0%; Pred. No. 1.5e-07;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VIFNYGKNVLINKDIRC 18  
|||||  
Db 129 VIFNYGKNVLINKDIRC 146

RESULT 2  
S06763  
calreticulin precursor - mouse  
N:Alternate names: 55K calcium-binding reticuloplasmin; calregulin  
C:Species: Mus musculus (house mouse)  
C:Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 10-Sep-1999  
C:Accession: S06763; JG1444; PC1233; A57498  
R:Smith, M.J.; Koch, G.L.E.  
EMBO J. 8, 3581-3586, 1989  
A:Title: Multiple zones in the sequence of calreticulin (CRP55, calregulin, HACBP), a  
A:Reference number: S06763; MUID:90059955  
A:Accession: S06763  
A:Molecule type: DNA

A:Residues: 1-416 <SMT>  
A:Cross-references: EMBL:X14926; NID:g50567; PIDN:CAA33053.1; PID:g50568  
R:Mazzarolli, R.A.; Gold, P.; Cunningham, M.; Green, M.  
Gene 120, 217-225, 1992  
A:Title: Determination of the sequence of an expressible cDNA clone encoding Erp60/calnexin  
A:Reference number: JC1444; MUID:93013037  
A:Accession: JC1444  
A:Molecule type: mRNA  
A:Residues: 1-416 <MAZ>  
A:Cross-references: GB:M92988; NID:g193084; PIDN:AAA37569.1; PID:g193085  
A:Accession: PC1233  
A:Molecule type: protein  
A:Residues: 18-41 <MAZ>  
R:White, T.K.; Zhu, Q.; Tanzer, M.L.  
J. Biol. Chem. 270, 15926-15929, 1995  
A:Title: Cell surface calreticulin is a putative mannoside lectin which triggers mouse m...  
A:Reference number: A57498; MUID:95332280  
A:Accession: A57498  
A>Status: preliminary  
A:Molecule type: protein  
A:Residues: 74-80;142-151;186-193 <WHI>  
C:Superfamily: calreticulin  
C:Keywords: calcium binding  
F:1-17/Domain: signal sequence #status predicted <SIG>  
F:18-416/Product: calreticulin #status experimental <MAT>  
F:413-416/Region: endoplasmic reticulum retention signal

Query Match 100.0%; Score 96; DB 1; Length 416;  
Best Local Similarity 100.0%; Pred. No. 1.5e-07;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VIFNYKGNVLINKDIRC 18  
|||||  
DB 146 VIFNYKGNVLINKDIRC 163

RESULT 3  
JH0819  
calreticulin precursor - rat  
N:Alternate names: calcium-binding protein 3  
C:Species: Rattus norvegicus (Norway rat)  
C:Date: 30-Sep-1993 #sequence\_revision 20-Aug-1994 #text\_change 20-Jun-2000  
A:Accession: JH0819; A9176; S11205; PC1109; S45036; S04867; S39372; A34473; S13045  
R:Nakamura, M.; Moriya, M.; Baba, T.; Michikawa, Y.; Yananobe, T.; Arai, K.; Okinaga, S.  
Exp. Cell Res. 205, 101-110, 1993  
A:Title: An endoplasmic reticulum protein, calreticulin, is transported into the acrosome  
A:Reference number: A49176; MUID:93202172  
A:Accession: JH0819  
A:Molecule type: mRNA  
A:Residues: 1-416 <NAK>  
A:Cross-references: GB:D78308; NID:g1089798; PIDN:BAAL1345.1; PID:g1845572  
A:Accession: A49176  
A>Status: preliminary  
A:Molecule type: protein  
A:Residues: 1-416 <NAK>  
A:Cross-references: GB:D78308; NID:g1089798; PIDN:BAAL1345.1; PID:g1845572  
A:Experimental source: Sprague-Dawley, spermatogenic cells  
A:Note: sequence extracted from NCBI backbone (NCBIN:127639, NCBIP:127643)  
R:Murthy, K.K.; Banville, D.; Srikant, C.B.; Carrier, F.; Holmes, C.; Bell, A.; Patel, Y.  
Nucleic Acids Res. 18, 4933, 1990  
A:Title: Structural homology between the rat calreticulin gene product and the Onchocerca  
A:Reference number: S11205; MUID:90370496  
A:Accession: S11205  
A:Molecule type: mRNA  
A:Residues: 1-416 <MUR>  
A:Cross-references: EMBL:X53363; NID:g55854; PIDN:CAA37446.1; PID:g55855  
R:Nakamura, M.; Michikawa, Y.; Baba, T.; Okinaga, S.; Arai, K.  
Biochem. Biophys. Res. Commun. 186, 668-673, 1992  
A:Title: Calreticulin is present in the acrosome of spermatozoa of rat testis.  
A:Reference number: PC1109; MUID:92360010  
A:Accession: PC1109  
A:Molecule type: protein

A:Residues: 18-32 <NAK>  
A:Experimental source: testis, strain Sprague-Dawley  
R:Soenichsen, B.; Fuellekrug, J.; van Nguyen, P.; Diekmann, W.; Robinson, D.G.; Mies  
submitted to the EMBL Data Library, May 1994  
A:Description: Retention and retrieval: both mechanisms cooperate to maintain calretic  
A:Reference number: S45036  
A:Accession: S45036  
A>Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-416 <SOE>  
A:Cross-references: EMBL:X79327; NID:g488840; PIDN:CAA55890.1; PID:g488841  
R:Lone, Y.C.; Bailly, A.; Latruffe, N.  
submitted to the EMBL Data Library, December 1988  
A:Reference number: S04867  
A:Accession: S04867  
A:Molecule type: mRNA  
A:Residues: 'R',270-358,'AAG',<LON>  
A:Cross-references: EMBL:X13702; NID:g56055; PIDN:CAA31987.1; PID:g930260  
A:Note: the authors designated the protein as D-beta-hydroxybutyrate dehydrogenase  
R:Yokoi, T.; Nagayama, S.; Kajiwara, R.; Kawaguchi, Y.; Horiuchi, R.; Kanataki, T.  
Biochim. Biophys. Acta 1158, 339-344, 1993  
A:Title: Identification of protein disulfide isomerase and calreticulin as autoimmune  
A:Reference number: S39371; MUID:94072621  
A:Accession: S39372  
A:Molecule type: protein  
A:Residues: 18-23,'X',25-32 <VOK>  
R:Van, P.N.; Peter, F.; Soeling, H.D.  
J. Biol. Chem. 264, 17494-17501, 1989  
A:Title: Four intracisternal calcium-binding glycoproteins from rat liver microsomes  
A:Reference number: A34473; MUID:90008920  
A:Accession: A34473  
A>Status: preliminary  
A:Molecule type: protein  
A:Residues: 18-36 <VAN>  
R:Trevies, S.; de Mattei, M.; Lanfredi, M.; Villa, A.; Green, N.M.; MacLennan, D.H.; M  
Biochem. J. 271, 473-480, 1990  
A:Title: Calreticulin is a candidate for a calsequestrin-like function in Ca(2+)-stor  
A:Reference number: S13045; MUID:91054414  
A:Accession: S13045  
A:Molecule type: protein  
A:Residues: 18-29 <TRE>  
C:Superfamily: calreticulin  
C:Keywords: calcium binding; glycoprotein  
F:1-17/Domain: signal sequence #status predicted <SIG>  
F:18-416/Product: calreticulin #status experimental <MAT>  
F:204-212/Region: nuclear location signal  
F:413-416/Region: endoplasmic reticulum retention signal  
F:344/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 100.0%; Score 96; DB 2; Length 416;  
Best Local Similarity 100.0%; Pred. No. 1.5e-07;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VIFNYKGNVLINKDIRC 18  
|||||  
DB 146 VIFNYKGNVLINKDIRC 163

RESULT 4  
A37047  
calreticulin precursor - human  
N:Alternate names: 52K ribonucleoprotein autoantigen Ro/SS-A; 60K integrin-binding pr  
C:Species: Homo sapiens (man)  
C:Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 18-Feb-2000  
A:Accession: A42330; A37047; A46452; A28812; PH1525; A40346; S11475; T45075  
R:McCaulliffe, D.P.; Yang, Y.S.; Wilson, J.; Sontheimer, R.D.; Capra, J.D.  
J. Biol. Chem. 267, 2557-2562, 1992  
A:Title: The 5'-flanking region of the human calreticulin gene shares homology with t  
A:Reference number: A42330; MUID:92129342  
A:Accession: A42330  
A:Molecule type: DNA



A:Residues: 1-417 <MC2>  
A:Note: sequence extracted from NCBI backbone (NCBIN:78537, NCBIP:78536)  
R:McCaulliffe, D.P.; Lux, F.A.; Lieu, T.S.; Sanz, I.; Hanke, J.; Newkirk, M.M.; Bachinski  
J. Clin. Invest. 85, 1379-1391, 1990  
A:Title: Molecular cloning, expression, and chromosome 19 localization of a human Ro/SS-  
A:Reference number: A37047; MUID:90237213  
A:Accession: A37047  
A:Molecule type: mRNA  
A:Residues: 1-417 <MC2>  
A:Cross-references: GB:M32294; NID:9337486; PIDN:AAA36582.1; PID:9337487  
A:Note: the authors translated the codon GTA for residue 349 as Tyr  
R:Roekach, L.A.; Haselby, J.A.; Meliof, J.F.; Smeenk, R.J.; Unnasch, T.R.; Greene, B.M.;  
J. Immunol. 147, 3031-3039, 1991  
A:Title: Characterization of the autoantigen calreticulin.  
A:Reference number: A46452; MUID:92013129  
A:Accession: A46452  
A:Molecule type: mRNA  
A:Residues: 1-417 <ROK>  
A:Cross-references: GB:M84739; NID:q179881; PIDN:AAA51916.1; PID:q179882  
A:Note: sequence extracted from NCBI backbone (NCBIN:60749, NCBIP:60750)  
R:Lieu, T.S.; Newkirk, M.M.; Capra, J.D.; Sontheimer, R.D.  
J. Clin. Invest. 82, 96-101, 1988  
A:Title: Molecular characterization of human Ro/SS-A antigen. Amino terminal sequence of  
A:Reference number: A28812; MUID:88273610  
A:Accession: A28812  
A:Molecule type: protein  
A:Residues: 18-41 <LIE>  
A:Note: 18-Ala was also found  
R:Dupuis, M.; Schaefer, E.; Krause, K.H.; Tschopp, J.  
J. Exp. Med. 177, 1-7, 1993  
A:Title: The calcium-binding protein calreticulin is a major constituent of lytic granul  
A:Reference number: PH1525; MUID:93115648  
A:Accession: PH1525  
A:Molecule type: protein  
A:Residues: 18-27 <DUP>  
A:Experimental source: LAK cell  
R:Nojima, M.V.; Finlay, B.B.; Gray, V.; Dedhar, S.  
Biochemistry 30, 9859-9866, 1991  
A:Title: In vitro interaction of a polypeptide homologous to human Ro/SS-A antigen (calr  
A:Reference number: A40346; MUID:92002034  
A:Accession: A40346  
A:Molecule type: protein  
A:Residues: 18-34, R' <ROU>  
R:Krause, K.H.; Simmerman, H.K.B.; Jones, L.R.; Campbell, K.P.  
Biochem. J. 270, 545-548, 1990  
A:Title: Sequence similarity of calreticulin with a Ca(2+)-binding protein that co-purif  
A:Reference number: S11475; MUID:90380058  
A:Accession: S11475  
A:Molecule type: protein  
A:Residues: 18-32 <KRA>  
R:Lamerdin, J.; McCready, P.; Stilwagen, S.; Ramirez, M.; Carrano, A.  
submitted to the EMBL Data Library, November 1996  
A:Description: Characterization by genomic sequence analysis of a gene-rich 111 kb regio  
A:Reference number: 222906  
A:Accession: T45075  
A>Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-417 <LAM>  
A:Cross-references: EMBL:AD000092; PIDN:AA851176.1  
A:Experimental source: cell line 5H12-B; fibroblast  
C:Comment: Autoantibodies specific for this protein are found in Sjogren's syndrome and  
C:Genetics:  
A:Gene: GDB:CALR  
A:Cross-references: GDB:125179; OMIM:109091  
A:Map position: 19p13.3-19p13.2  
A:Introns: 31/1; 65/1; 135/1; 164/3; 234/3; 272/3; 320/3; 351/3  
A:Note: CRTG  
C:Superfamily: calreticulin  
C:Keywords: calcium binding; integrin binding  
F:1-17/Domain: signal sequence #status predicted <SIG>  
F:18-417/Product: calreticulin #status predicted <MAT>  
F:414-417/Region: endoplasmic reticulum retention signal

Query Match 100.0%; Score 96; DB 1; Length 417;  
Best Local Similarity 100.0%; Pred. No. 1.5e-07;  
Matches 18; Conservative 0; Mismatches 0; Gaps 0;

QY 1 VIFNYGKGNVLINKDIRC 18  
|||||  
DB 146 VIFNYGKGNVLINKDIRC 163

## RESULT 5

A34154  
calreticulin precursor, skeletal muscle - rabbit  
C:Species: Oryctolagus cuniculus (domestic rabbit)  
C:Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 10-Sep-1999  
C:Accession: A34154; S13047  
R:Fliegel, L.; Burns, K.; MacLennan, D.H.; Reithmeier, R.A.F.; Michalak, M.  
J. Biol. Chem. 264, 21522-21528, 1989  
A:Title: Molecular cloning of the high affinity calcium-binding protein (calreticulin  
A:Reference number: A34154; MUID:90094320  
A:Accession: A34154  
A>Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-418 <FLI>  
A:Cross-references: GB:J05138; NID:q164858; PIDN:AAA31188.1; PID:q164859  
R:Freves, S.; de Mattei, M.; Lanfredi, M.; Villa, A.; Green, N.M.; MacLennan, D.H.; M  
Biochem. J. 271, 473-480, 1990  
A:Title: Calreticulin is a candidate for a calsequestrin-like function in Ca(2+)-stor  
A:Reference number: S13045; MUID:91054414  
A:Accession: S13047  
A:Molecule type: protein  
A:Residues: 19-32 <TRE>  
C:Superfamily: calreticulin  
C:Keywords: skeletal muscle  
F:1-17/Domain: signal sequence #status predicted <SIG>  
F:415-418/Region: endoplasmic reticulum retention signal

Query Match 100.0%; Score 96; DB 1; Length 418;  
Best Local Similarity 100.0%; Pred. No. 1.5e-07;  
Matches 18; Conservative 0; Mismatches 0; Gaps 0;

QY 1 VIFNYGKGNVLINKDIRC 18  
|||||  
DB 146 VIFNYGKGNVLINKDIRC 163

## RESULT 6

S36799  
calreticulin precursor, brain isoform 2 - bovine  
C:Species: Bos primigenius taurus (cattle)  
C:Date: 10-Dec-1993 #sequence\_revision 23-Mar-1995 #text\_change 13-Aug-1999  
C:Accession: S36799; S36800  
R:Liu, N.; Fine, R.E.; Johnson, R.J.  
Biochim. Biophys. Acta 1202, 70-76, 1993  
A:Title: Comparison of cDNAs from bovine brain coding for two isoforms of calreticuli  
A:Reference number: S36799; MUID:93385184  
A:Accession: S36799  
A:Molecule type: mRNA  
A:Residues: 1-421 <LIU>  
A:Cross-references: GB:LI13462; NID:g348693; PIDN:AAC37307.1; PID:g348694  
A:Experimental source: brain, clone 9.4  
A:Accession: S36800  
A:Molecule type: protein  
A:Residues: 35-45 <LI2>  
C:Superfamily: calreticulin  
C:Keywords: calcium binding; glycoprotein  
F:1-34/Domain: signal sequence #status predicted <SIG>  
F:35-421/Product: calreticulin, brain isoform 2 #status predicted <MAT>  
F:418-421/Region: endoplasmic reticulum retention signal  
F:141-167/Disulfide bonds: #status predicted  
F:183/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 100.0%; Score 96; DB 2; Length 421;  
 Best Local Similarity 100.0%; Pred. No. 1.5e-07;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VIFNYGKGNVLINKDIRC 18  
 ||||| ||||| ||||| |||||  
 Db 150 VIFNYGKGNVLINKDIRC 167

RESULT 7  
 JH0795  
 calreticulin precursor - California sea hare  
 N:Alternate names: protein 407  
 C:Species: Aplysia californica (California sea hare)  
 C>Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 10-Sep-1999  
 C:Accession: JH0795; B31409; F60977  
 R:Kennedy, T.E.; Kuhl, D.; Barzilai, A.; Sweatt, J.D.; Kandel, E.R.  
 Proc. Natl. Acad. Sci. U.S.A. 85; 7008-7012, 1988  
 A:Title: Long-term sensitization training in aplysia leads to an increase in calreticulin  
 A:Reference number: JH0795; MUID:93098937  
 A:Accession: JH0795  
 A:Molecule type: mRNA  
 A:Residues: 1-405 <KEN>  
 A:Cross-references: GB:S51239; NID:G262053; PIDN:AAB24569.1; PID:G262054  
 A:Experimental source: abdominal ganglion and antral nervous system  
 R:Kennedy, T.E.; Gawinowicz, M.A.; Barzilai, A.; Kandel, E.R.; Sweatt, J.D.  
 Proc. Natl. Acad. Sci. U.S.A. 85; 7008-7012, 1988  
 A:Title: Sequencing of proteins from two-dimensional gels by using in situ digestion and  
 tion in Aplysia.  
 A:Reference number: A94207; MUID:88320566  
 A:Accession: B31409  
 A:Molecule type: protein  
 A:Residues: 'X',17-28,'X',30-31 <KE>  
 R:Sweatt, J.D.; Kennedy, T.E.; Wager-Smith, K.; Gawinowicz, M.A.; Barzilai, A.; Karl, K.  
 Electrophoresis 10, 152-157, 1989  
 A:Title: Development of a database of amino acid sequences for proteins identified and  
 A:Reference number: A60977; MUID:89276264  
 A:Accession: F60977  
 A:Molecule type: protein  
 A:Residues: 'X',17-28,'X',30-31 <SW>  
 C:Superfamily: calreticulin  
 C:Keywords: calcium binding; endoplasmic reticulum  
 F:1-15/Domain: signal sequence #status predicted <SIG>  
 F:16-405/Product: calreticulin #status experimental <MAT>  
 F:402-405/Region: endoplasmic reticulum retention signal

Query Match 89.6%; Score 86; DB 1; Length 405;  
 Best Local Similarity 83.3%; Pred. No. 5.7e-06;  
 Matches 15; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 VIFNYGKGNVLINKDIRC 18  
 ||||| ||||| ||||| |||||  
 Db 142 VIFNYGKGNLLVKKDIRC 159

RESULT 8  
 A56637  
 calreticulin homolog precursor - fruit fly (Drosophila melanogaster)  
 N:Alternate names: Ro/SS-A autoantigen/calreticulin homolog  
 C:Species: Drosophila melanogaster  
 C>Date: 11-Aug-1995 #sequence\_revision 11-Aug-1995 #text\_change 13-Aug-1999  
 C:Accession: A56637; A37158  
 R:Smith, M.J.  
 DNA Seq. 3, 247-250, 1992  
 A:Title: Nucleotide sequence of a Drosophila melanogaster gene encoding a calreticulin h  
 A:Reference number: A56637; MUID:93208374  
 A:Accession: A56637  
 A>Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-406 <SMI>  
 A:Cross-references: GB:X64461; NID:g7685; PIDN:CAA5791.1; PID:g7686

A:Note: sequence extracted from NCBI backbone (NCBIN:128274, NCBI:128275)  
 R:McCaulliffe, D.P.; Zappi, E.; Lieu, T.S.; Michalak, M.; Sontheimer, R.D.; Capra, J.D.  
 J. Clin. Invest. 86, 332-335, 1990  
 A:Title: A human Ro/SS-A autoantigen is the homologue of calreticulin and is highly h  
 A:Reference number: A37158; MUID:90307981  
 A:Accession: A37158  
 A>Status: preliminary; nucleic acid sequence not shown; not compared with conceptual  
 A:Molecule type: DNA  
 A:Residues: 91-105,'A',107,109-124;182-183,'L',185-220 <MCC>  
 C:Genetics:  
 A:Gene: FlyBase:Crc  
 A:Cross-references: FlyBase:FBgn0005585  
 A:Introns: 65/1; 222/3  
 C:Superfamily: calreticulin  
 C:Keywords: calcium binding; endoplasmic reticulum  
 F:1-17/Domain: signal sequence #status predicted <SIG>  
 F:403-406/Region: endoplasmic reticulum retention signal

Query Match 82.3%; Score 79; DB 2; Length 406;  
 Best Local Similarity 83.3%; Pred. No. 7.3e-05;  
 Matches 15; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 VIFNYGKGNVLINKDIRC 18  
 ||||| ||||| ||||| |||||  
 Db 146 VIFSYGKGNHLISKDIRC 163

RESULT 9  
 S71343  
 calreticulin precursor - Korean frog  
 C:Species: Rana rugosa (Korean frog)  
 C>Date: 29-Jan-1998 #sequence\_revision 13-Feb-1998 #text\_change 20-Jun-2000  
 C:Accession: S71343  
 R:Yamamoto, S.; Nakamura, M.  
 FEBS Lett. 387, 27-32, 1996  
 A:Title: Calnexin: its molecular cloning and expression in the liver of the frog, Ran  
 A:Reference number: S71342; MUID:96234004  
 A:Accession: S71343  
 A>Status: nucleic acid sequence not shown  
 A:Molecule type: mRNA  
 A:Residues: 1-419 <AM>  
 A:Cross-references: EMBL:D78589; NID:g1514956; PIDN:BAA11425.1; PID:g1514957  
 C:Superfamily: calreticulin  
 C:Keywords: calcium binding; endoplasmic reticulum  
 F:1-18/Domain: signal sequence #status predicted <SIG>  
 F:19-419/Product: calreticulin #status predicted <MAT>  
 F:205-213/Region: nuclear location signal  
 F:415-418/Region: endoplasmic reticulum retention signal

Query Match 81.2%; Score 78; DB 2; Length 419;  
 Best Local Similarity 88.2%; Pred. No. 0.00011;  
 Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 VIFNYGKGNVLINKDIR 17  
 ||||| ||||| ||||| |||||  
 Db 147 VIFNYGKGNLQINKDIR 163

RESULT 10  
 S29130  
 calreticulin (clone 8) - African clawed frog (fragment)  
 C:Species: Xenopus laevis (African clawed frog)  
 C>Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 13-Aug-1999  
 C:Accession: S29130; T01068  
 R:Treves, S.; Zorzato, F.; Pozzan, T.  
 Biochem. J. 287, 579-581, 1992  
 A:Title: Identification of calreticulin isoforms in the central nervous system.  
 A:Reference number: S29129; MUID:93074997  
 A:Accession: S29130  
 A:Molecule type: mRNA  
 A:Residues: 1-384 <TRE>

A:Cross-references: EMBL:X67598  
A:Accession: T01068

A:Status: translated from GB/EMBL/DBDJ

A:Molecule type: mRNA

A:Residues: 1-339, 'XTCGR' <TRW>

A:Cross-references: EMBL:X67598; NID:g64610; PIDN:CAA47867.1; PID:g64611

A:Experimental source: CNS

C:Superfamily: calreticulin

C:Keywords: glycoprotein

F:381-384/Region: endoplasmic reticulum retention signal

F:316/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 76.0%; Score 73; DB 2; Length 384;

Best Local Similarity 77.8%; Pred. No. 0.00062;

Matches 14; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 VIFNYKGNVLINKDIRC 18

||||| ||| ||| ||| |||

DB 118 VIFQYKKRNQLINKDIRC 135

RESULT 11

S29129

calreticulin precursor (clone 3) - African clawed frog (fragment)

C:Species: Xenopus laevis (African clawed frog)

C:Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 13-Aug-1999

C:Accession: S29129

R:Treves, S.; Zorzato, F.; Pozzan, T.

Biochem. J. 287, 579-581, 1992

A:Title: Identification of calreticulin isoforms in the central nervous system.

A:Reference number: S29129; MUID:93074997

A:Accession: S29129

A:Molecule type: mRNA

A:Residues: 1-411 <TRE>

A:Cross-references: EMBL:X67597; NID:g64608; PIDN:CAA47866.1; PID:g64609

C:Superfamily: calreticulin

C:Keywords: glycoprotein

F:1-12/Domain: signal sequence (fragment) #status predicted <SIG>

F:13-411/Product: calreticulin #status predicted <MAT>

F:408-411/Region: endoplasmic reticulum retention signal

F:339/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 76.0%; Score 73; DB 2; Length 411;

Best Local Similarity 77.8%; Pred. No. 0.00066;

Matches 14; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 VIFNYKGNVLINKDIRC 18

||||| ||| ||| ||| |||

DB 141 VIFQYKKRNQLINKDIRC 158

RESULT 12

A48573

calreticulin autoantigen homolog precursor - fluke (Schistosoma mansoni)

C:Species: Schistosoma mansoni

C:Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 10-Sep-1999

C:Accession: A48573

R:Khalife, J.; Trottein, F.; Schacht, A.M.; Godin, C.; Pierce, R.J.; Capron, A.

Mol. Biochem. Parasitol. 57, 193-202, 1993

A:Title: Cloning of the gene encoding a Schistosoma mansoni antigen homologous to human

A:Reference number: A48573; MUID:93165070

A:Accession: A48573

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-393 <KHA>

A:Cross-references: GB:M93097; NID:g160928

A:Note: sequence inconsistent with the nucleotide translation

C:Superfamily: calreticulin

F:1-16/Domain: signal sequence #status predicted <SIG>

F:390-393/Region: endoplasmic reticulum retention signal

Query Match 75.0%; Score 72; DB 1; Length 393;

Best Local Similarity 77.8%; Pred. No. 0.00091;

Matches 14; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 VIFNYKGNVLINKDIRC 18

||||| ||| ||| ||| |||

DB 144 VIFNYKGNHLIKKEIPC 161

RESULT 13

A32507

41k larval antigen - nematode (Onchocerca volvulus) (fragment)

C:Species: Onchocerca volvulus

C:Date: 21-May-1990 #sequence\_revision 21-May-1990 #text\_change 12-Apr-1995

C:Accession: A32507; A28813

R:Unnasch, T.R.; Gallin, M.Y.; Soboslay, P.T.; Erttmann, K.D.; Greene, B.M.

J. Clin. Invest. 82, 262-269, 1988

A:Title: Isolation and characterization of expression cDNA clones encoding antigens o

A:Reference number: A92769; MUID:88273584

A:Accession: A32507

A:Molecule type: mRNA

A:Residues: 1-336 <ONN>

C:Superfamily: calreticulin

Query Match 68.8%; Score 66; DB 2; Length 336;

Best Local Similarity 66.7%; Pred. No. 0.0069;

Matches 12; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 VIFNYKGNVLINKDIRC 18

||||| ||| ||| ||| |||

DB 92 VIFHYKDRNHMIKKDIRC 109

RESULT 14

S25851

calreticulin precursor - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C:Date: 06-Jan-1994 #sequence\_revision 10-Nov-1995 #text\_change 05-Nov-1999

C:Accession: S25851; T33996

R:Smith, M.J.

DNA Seq. 2, 235-240, 1992

A:Title: A C. elegans gene encodes a protein homologous to mammalian calreticulin.

A:Reference number: S25851; MUID:92329978

A:Accession: S25851

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-395 <SMI>

A:Cross-references: EMBL:X59589; NID:g6693; PIDN:CAA42159.1; PID:g6694

R:Bauer, C.; Courtney, L.; Laplant, Y.

submitted to the EMBL Data Library, February 1999

A:Description: The sequence of C. elegans cosmid Y38A10A.

A:Reference number: 221453

A:Accession: T33996

A:Status: preliminary; translated from GB/EMBL/DBDJ

A:Molecule type: DNA

A:Residues: 1-395 <BAU>

A:Cross-references: EMBL:AF125963; PIDN:AAD14746.1; GSPDB:GN00023; CESP:Y38A10A.5

A:Experimental source: strain Bristol N2; clone Y38A10A

C:Genetics:

A:Gene: CESP:Y38A10A.5

A:Map position: 5

A:Introns: 107/3; 315/3

C:Superfamily: calreticulin

F:1-15/Domain: signal sequence #status predicted <SIG>

F:392-395/Region: endoplasmic reticulum retention signal

Query Match 66.7%; Score 64; DB 2; Length 395;

Best Local Similarity 66.7%; Pred. No. 0.017;

Matches 12; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 VIPNYGKNVINKDIRC 18  
 || ||||: || ||: |  
 Db 141 VILNYGKNKLINKEITC 158

RESULT 15  
 T14554  
 calreticulin - beet  
 C:Species: Beta vulgaris (beet)  
 C:Date: 20-Sep-1999 #sequence\_revision 20-Sep-1999 #text\_change 20-Jun-2000  
 C:Accession: T14554  
 K:Viereck, R.  
 submitted to the EMBL Data Library, October 1997  
 A:Description: Nucleotide sequence from sugar beet calreticulin.  
 A:Reference number: Z18137  
 A:Accession: T14554  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: mRNA  
 A:Residues: 1-416 <VIE>  
 A:Cross-references: EMBL:AJ002057  
 A:Experimental source: strain diploide Inzuchtlinie KWS; leaf  
 C:Superfamily: calreticulin  
 C:Keywords: calcium binding

Query Match 55.2%; Score 53; DB 2; Length 416;  
 Beet Local Similarity 58.8%; Pred. No. 0.98;  
 Matches 10; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 2 IFNYGKNVINKDIRC 18  
 |||| | || ||: |  
 Db 153 IFNYDTHLIKDVPC 169

Search completed: January 9, 2002, 15:02:03  
 Job time: 190 sec

GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: January 9, 2002, 15:03:28 ; Search time 78.15 Seconds  
(without alignments)  
50.536 Million cell updates/sec

Title: US-09-828-000-5  
Perfect score: 151  
Sequence: 1 CGPGTKKVVHVIENYKGNVLINKDIRC 27

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 473505 seqs, 146272329 residues

Total number of hits satisfying chosen parameters: 473505

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL17:\*  
1: sp\_archaea:\*  
2: sp\_bacteria:\*  
3: sp\_fungi:\*  
4: sp\_human:\*  
5: sp\_invertebrate:\*  
6: sp\_mammal:\*  
7: sp\_mhc:\*  
8: sp\_organelle:\*  
9: sp\_phase:\*  
10: sp\_plant:\*  
11: sp\_rodent:\*  
12: sp\_virus:\*  
13: sp\_vertebrate:\*  
14: sp\_unclassified:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	144	95.4	318	13	Q9PTX7
2	142	94.0	421	5	Q9U6S0
3	141	93.4	405	5	Q26268
4	140	92.7	410	5	Q16893
5	134	88.7	406	5	Q9U916
6	128	84.8	375	5	Q18478
7	128	84.8	387	5	Q97372
8	125	82.8	419	13	Q98984
9	120	79.5	343	13	Q91711
10	120	79.5	411	13	Q91710
11	115	76.2	417	13	Q9PUC1
12	109.5	72.5	403	5	Q76961
13	108	71.5	350	5	Q26514
14	108	71.5	396	5	Q45034
15	99	65.6	321	13	Q9U5G0
16	84	55.6	412	10	Q40040
17	84	55.6	415	10	Q40041
18	83	55.0	321	10	Q41799
19	83	55.0	421	10	Q43712

20	80.5	53.3	427	10	Q9FYV2	Q9fyv2 pinus taeda
21	80	53.0	422	10	Q22502	Q22502 brassica na
22	76	50.3	240	10	Q9ST29	Q9st29 solanum mel
23	76	50.3	389	10	Q40567	Q40567 nicotiana t
24	61	40.4	70	10	Q9SXW3	Q9sxw3 lithospermu
25	57	37.7	137	11	Q9D373	Q9d373 mus musculus
26	57	37.7	380	11	Q9D906	Q9d906 mus musculus
27	54	35.8	720	1	Q73946	Q73946 pyrococcus
28	53	35.1	764	2	Q9HXE0	Q9hxe0 pseudomonas
29	51	33.8	348	4	Q00557	Q00557 homo sapien
30	50.5	33.4	499	11	Q9DBB3	Q9dbb3 mus musculus
31	50	33.1	275	2	Q9A131	Q9a131 streptococc
32	50	33.1	304	3	Q00867	Q00867 neectria hae
33	50	33.1	708	5	Q9GVA7	Q9gva7 pimpla hypo
34	50	33.1	783	2	Q9LAW0	Q9law0 mycoplasma
35	49	32.5	434	12	Q69017	Q69017 ictaluriid h
36	49	32.5	506	13	Q73736	Q73736 brachydanio
37	49	32.5	506	13	Q9DGI6	Q9dgi6 brachydanio
38	49	32.5	654	12	Q9DUB1	Q9dub1 tt virus..o
39	48.5	32.1	89	2	P96636	P96636 bacillus su
40	48.5	32.1	1765	5	Q26791	Q26791 trypanosoma
41	48.5	32.1	1765	5	Q26794	Q26794 trypanosoma
42	48	31.8	183	1	Q28949	Q28949 archaeoglob
43	48	31.8	247	2	Q48830	Q48830 lactobacill
44	48	31.8	846	13	Q57577	Q57577 cynops pyrr
45	48	31.8	1100	13	O57576	O57576 cynops pyrr

#### ALIGNMENTS

RESULT 1

Q9PTX7 ID Q9PTX7 PRELIMINARY: PRT: 318 AA.  
AC Q9PTX7;  
DT 01-MAY-2000 (TRENBLrel. 13, Created)  
DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)  
DT 01-JUN-2001 (TRENBLrel. 17, Last annotation update)  
DE CALRETICULIN (FRAGMENT).  
OS Lampetra reissneri.  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Hyperoartia;  
OC Petromyzontiformes; Petromyzontidae; Lampetra.  
OX NCBI\_TaxID=7753;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=20063780; PubMed=10594174;  
RA Kuraku S., Hoshiyama D., Katoh K., Suga H., Miyata T.;  
RT "Monophyly of lampreys and hagfishes supported by nuclear DNA-coded genes";  
RL J. Mol. Evol. 49:729-735(1999).  
DR EMBL; AB025328; BAA88481.1; .  
DR InterPro; IPR000886; ER.target.  
DR InterPro; IPR001580; Calreticulin.  
DR Pfam; PF00262; calreticulin; 1.  
DR PRINTS; PR00626; CALRETICULIN.  
DR PRODOM; PD001866; Calreticulin; 1.  
DR PROSITE; PS00804; CALRETICULIN\_2; 1.  
DR PROSITE; PS00805; CALRETICULIN\_REPEAT; 3.  
DR PROSITE; PS00014; ER\_TARGET; UNKNOWN\_1.  
FT NON\_TER 1  
SQ SEQUENCE 318 AA: 36997 MW: C88102EA1CAC1506 CRC64;

Query Match 95.4%; Score 144; DB 13; Length 318;

Best Local Similarity 96.3%; Pred No. 1.3e-12;

Matches 26; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CGPGTKKVVHVIENYKGNVLINKDIRC 27

Db ||||| ||||| ||||| ||||| |||||

36 CGPGTKKVVHVIENYKGNVLINKDIRC 62

RESULT 2

## Q9U6S0

ID Q9U6S0 PRELIMINARY; PRT; 421 AA.  
 AC Q9U6S0;  
 DT 01-MAY-2000 (TReMBLrel. 13, Created)  
 DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)  
 DT 01-JUN-2001 (TReMBLrel. 17, Last annotation update)  
 DE CALRETICULIN PRECURSOR.  
 GN CALRET.  
 OS Strongylocentrotus purpuratus (Purple sea urchin).  
 OC Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;  
 OC Echinozoa; Echinoidae; Echinacea; Echinoidae; Strongylocentrotidae;  
 OC Strongylocentrotus.  
 OX NCBI\_TaxID 7668;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Susan J.M., Just M.L., Lennarz W.J.;  
 RT "Cloning and Characterization of AlphaP Integrin and Calreticulin in  
 Embryos of the Sea Urchin."  
 RL Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AF177915; AAD5725.1; -;  
 DR InterPro: IPR000886; ER\_target.  
 DR InterPro: IPR001580; Calreticulin.  
 DR Pfam: PF00262; calreticulin; 1.  
 DR PRINTS: PR00626; CALRETICULIN.  
 DR ProDom: PD001866; Calreticulin; 1.  
 DR PROSITE: PS00804; CALRETICULIN\_2; 1.  
 DR PROSITE: PS00805; CALRETICULIN\_REPEAT; 3.  
 DR PROSITE: PS00014; ER\_TARGET; UNKNOWN\_1.  
 KW Signal.  
 FT SIGNAL. 1 19 POTENTIAL.  
 FT CHAIN 20 421 CALRETICULIN.  
 SQ SEQUENCE 421 AA; 48822 MW; 172C664F59F41F93 CRC64;

Query Match 94.0%; Score 142; DB 5; Length 421;

Best Local Similarity 92.6%; Pred. No. 3.5e-12;  
 Matches 25; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 CGPGTKKVVHVIENYKGNVLINKDIRC 27

Db 136 CGPGTKKVVHVIENYKGNVLINKDIRC 162

## RESULT 3

ID Q26268 PRELIMINARY; PRT; 405 AA.  
 AC Q26268;  
 DT 01-NOV-1996 (TReMBLrel. 01, Created)  
 DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)  
 DT 01-JUN-2001 (TReMBLrel. 17, Last annotation update)  
 DE CALRETICULIN  
 OS Aplysia californica (California sea hare).  
 OC Eukaryota; Metazoa; Mollusca; Gastropoda; Opisthobranchia; Anasplidea;  
 OC Aplysiidae; Aplysia.  
 OX NCBI\_TaxID 6500;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Kennedy T.E., Kuhl D., Barzilai A., Sweatt J.D., Kandel E.R.;  
 RT "Long-term sensitization training in Aplysia leads to an increase in  
 calreticulin, a major presynaptic calcium-binding protein.";  
 RL Neuron 9:1013-1024(1992).  
 DR EMBL: S51239; AAB24569.1; -;  
 DR InterPro: IPR000886; ER\_target.  
 DR InterPro: IPR001580; Calreticulin.  
 DR Pfam: PF00262; calreticulin; 1.  
 DR PRINTS: PR00626; CALRETICULIN.  
 DR ProDom: PD001866; Calreticulin; 1.  
 DR PROSITE: PS00803; CALRETICULIN\_1; 1.  
 DR PROSITE: PS00804; CALRETICULIN\_2; 1.  
 DR PROSITE: PS00805; CALRETICULIN\_REPEAT; 3.  
 DR PROSITE: PS00014; ER\_TARGET; UNKNOWN\_1.  
 SQ SEQUENCE 405 AA; 46738 MW; 14CAA201840DID69 CRC64;

Query Match 93.4%; Score 141; DB 5; Length 405;

Best Local Similarity 88.9%; Pred. No. 4.6e-12;  
 Matches 24; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 CGPGTKKVVHVIENYKGNVLINKDIRC 27

Db 133 CGPGTKKVVHVIENYKGNVLINKDIRC 159

## RESULT 4

ID Q16893 PRELIMINARY; PRT; 410 AA.  
 AC Q16893;  
 DT 01-NOV-1996 (TReMBLrel. 01, Created)  
 DT 01-JAN-1999 (TReMBLrel. 09, Last sequence update)  
 DT 01-JUN-2001 (TReMBLrel. 17, Last annotation update)  
 DE CALRETICULIN.  
 GN CRT-1.  
 OS Amblyomma americanum.  
 OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Acari;  
 OC Parasitiformes; Ixodida; Ixodidae; Amblyomma.  
 OX NCBI\_TaxID 6943;  
 RN [1]  
 RP SEQUENCE OF 49-410 FROM N.A.  
 RC TISSUE-SALIVARY GLANDS;  
 RA Jaworski D.C., Simmen F.A., Lamoreaux W.J., Coons L.B., Muller M.T.,  
 RA Needham G.R.;  
 RT "A secreted calreticulin protein in Ixodid tick (Amblyomma americanum)  
 saliva."  
 RL J. Insect Physiol. 41:369-375(1995).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE-SALIVARY GLANDS;  
 RA Jaworski D.C.;  
 RL Submitted (MAR-1994) to the EMBL/GenBank/DBJ databases.  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE-SALIVARY GLANDS;  
 RA Fain-Thornton J.M., Jaworski D.C., Needham G.R.;  
 RL Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: U07708; AAC79094.1; -;  
 DR InterPro: IPR000886; ER\_target.  
 DR InterPro: IPR001580; Calreticulin.  
 DR Pfam: PF00262; calreticulin; 1.  
 DR PRINTS: PR00626; CALRETICULIN.  
 DR ProDom: PD001866; Calreticulin; 1.  
 DR PROSITE: PS00803; CALRETICULIN\_1; 1.  
 DR PROSITE: PS00805; CALRETICULIN\_REPEAT; 3.  
 DR PROSITE: PS00014; ER\_TARGET; UNKNOWN\_1.  
 SQ SEQUENCE 410 AA; 47485 MW; 32CCB8750A17DC54 CRC64;

Query Match 92.7%; Score 140; DB 5; Length 410;

Best Local Similarity 92.6%; Pred. No. 6.5e-12;  
 Matches 25; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 CGPGTKKVVHVIENYKGNVLINKDIRC 27

Db 136 CGPGTKKVVHVIENYKGNVLINKDIRC 162

## RESULT 5

ID Q9U916 PRELIMINARY; PRT; 406 AA.  
 AC Q9U916;  
 DT 01-MAY-2000 (TReMBLrel. 13, Created)  
 DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)  
 DT 01-JUN-2001 (TReMBLrel. 17, Last annotation update)  
 DE CALRETICULIN.  
 GN CRC OR CG9429.  
 OS Drosophila melanogaster (Fruit fly).

RESULT 7  
O97372  
ID O97372 PRELIMINARY: PRT: 387 AA:





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ID 076961 PRELIMINARY; PRT; 403 AA.
AC 076961;
DT 01-NOV-1998 (TReMBLrel. 08, Created)
DT 01-NOV-1998 (TReMBLrel. 08, Last sequence update)
DT 01-JUN-2001 (TReMBLrel. 17, Last annotation update)
DE CALRETICULIN PRECURSOR.
GN CRT.
OS Necator americanus.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Strongylida;
OC Ancylostomatoidae; Ancylostomatidae; Bunostominae; Necator.
OX NCBI_TaxID=51031;
RN [1]
RP SEQUENCE FROM N.A.
RA Pritchard D.I., Brown A., McElroy P., Loukas A., Girdwood K.,
RA Berry C., Fullkrug R., Beck E.;
RT "Calreticulin is a hookworm allergen.";
RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ006790; CAA07254.1; -
DR InterPro; IPR000886; ER_target.
DR InterPro; IPR001580; Calreticulin.
DR Pfam; PF00262; calreticulin; 1.
DR PRINTS; PR00626; CALRETICULIN.
DR PRODOM; PD001866; Calreticulin; 1.
DR PROSITE; PS00803; CALRETICULIN_1; 1.
DR PROSITE; PS00804; CALRETICULIN_2; 1.
DR PROSITE; PS00805; CALRETICULIN_REPEAT; 3.
DR PROSITE; PS00014; ER_TARGET; UNKNOWN_1.
KW Signal; Allergen.
FT SIGNAL 1 16 POTENTIAL.
SQ SEQUENCE 403 AA; 46833 MW; 21F38B0515487B6F CRC64;

Query Match 72.5%; Score 109.5; DB 5; Length 403;
Best Local Similarity 81.5%; Pred. No. 1.4e-07;
Matches 22; Conservative 1; Mismatches 3; Indels 1; Gaps 1;

QY 1 CGPGTKKHVHVFNYKGNVLINKDIRC 27
||| ||||| ||||| ||||| ||||| |||||
DB 134 CGP-TKKVHDFSYKGNHLIKKDIRC 159

RESULT 13
Q26514 PRELIMINARY; PRT; 350 AA.
AC Q26514;
DT 01-NOV-1996 (TReMBLrel. 01, Created)
DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)
DT 01-JUN-2001 (TReMBLrel. 17, Last annotation update)
DE CALRETICULIN (FRAGMENT).
GN RAL-1.
OS Schistosoma japonicum (Blood fluke).
OC Eukaryota; Metazoa; Platyhelminthes; Rhabditophora; Neodermata;
OC Trematoda; Digenea; Strigeidida; Schistosomatoidae; Schistosomatidae;
OC Schistosoma.
OX NCBI_TaxID=6182;
RN [1]
RP SEQUENCE FROM N.A.
RA Huggins M.C., Moloney N.A.;
RL Submitted (AUG-1993) to the EMBL/GenBank/DBJ databases.
DR EMBL; M80524; AAA29917.1; -
DR InterPro; IPR000886; ER_target.
DR InterPro; IPR001580; Calreticulin.
DR Pfam; PF00262; calreticulin; 1.
DR PRINTS; PR00626; CALRETICULIN.
DR PRODOM; PD001866; Calreticulin; 1.
DR PROSITE; PS00803; CALRETICULIN_1; 1.
DR PROSITE; PS00804; CALRETICULIN_2; 1.
DR PROSITE; PS00805; CALRETICULIN_REPEAT; 1.
DR PROSITE; PS00014; ER_TARGET; UNKNOWN_1.
FT NON_TER 1
SQ SEQUENCE 350 AA; 40385 MW; 30FAB4E8BB685D1C CRC64;

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Query Match 71.5%; Score 108; DB 5; Length 350;
Best Local Similarity 70.4%; Pred. No. 1.9e-07;
Matches 19; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 1 CGPGTKKHVHVFNYKGNVLINKDIRC 27
||| ||||| ||||| ||||| ||||| |||||
DB 90 CGMATKRIHVIFNYKGNHLIKKDIRC 116

RESULT 14
Q45034 PRELIMINARY; PRT; 396 AA.
AC Q45034;
DT 01-JUN-1998 (TReMBLrel. 06, Created)
DT 01-JUN-1998 (TReMBLrel. 06, Last sequence update)
DT 01-JUN-2001 (TReMBLrel. 17, Last annotation update)
DE CALRETICULIN.
OS Schistosoma japonicum (Blood fluke).
OC Eukaryota; Metazoa; Platyhelminthes; Rhabditophora; Neodermata;
OC Trematoda; Digenea; Strigeidida; Schistosomatoidae; Schistosomatidae;
OC Schistosoma.
OX NCBI_TaxID=6182;
RN [1]
RP SEQUENCE FROM N.A.
RA Scott J.C.;
RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF044408; AAC00515.1; -
DR InterPro; IPR000886; ER_target.
DR InterPro; IPR001580; Calreticulin.
DR Pfam; PF00262; calreticulin; 1.
DR PRINTS; PR00626; CALRETICULIN.
DR PRODOM; PD001866; Calreticulin; 1.
DR PROSITE; PS00803; CALRETICULIN_1; 1.
DR PROSITE; PS00804; CALRETICULIN_2; 1.
DR PROSITE; PS00805; CALRETICULIN_REPEAT; 2.
DR PROSITE; PS00014; ER_TARGET; UNKNOWN_1.
SQ SEQUENCE 396 AA; 45813 MW; C57394C6FB4CD77B CRC64;

Query Match 71.5%; Score 108; DB 5; Length 396;
Best Local Similarity 70.4%; Pred. No. 2.2e-07;
Matches 19; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 1 CGPGTKKHVHVFNYKGNVLINKDIRC 27
||| ||||| ||||| ||||| ||||| |||||
DB 136 CGMATKRIHVIFNYKGNHLIKKDIRC 162

RESULT 15
Q9U5G0 PRELIMINARY; PRT; 321 AA.
AC Q9U5G0;
DT 01-MAY-2000 (TReMBLrel. 13, Created)
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TReMBLrel. 17, Last annotation update)
DE CALRETICULIN (FRAGMENT).
OS Eptatretus burgeri (Inshore hagfish).
OC Eukaryota; Metazoa; Chordata; Craniata; Hyperotreti; Myxiniiformes;
OC Myxiniidae; Eptatretinae; Eptatretus.
OX NCBI_TaxID=7764;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=LIVER;
RX MEDLINE=20063780; PubMed=10594174;
RA Kuraku S., Hoshiyama D., Katoh K., Suga H., Miyata T.;
RT "Monophyly of lampreys and hagfishes supported by nuclear DNA-coded
genes.";
RL J. Mol. Evol. 49:729-735(1999).
DR EMBL; AB025323; BAA88476.1; -
DR InterPro; IPR000886; ER_target.
DR InterPro; IPR001580; Calreticulin.

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DR Pfam: PF00262; calreticulin; 1.  
DR PRINTS: PR00626; CALRETICULIN.  
DR ProDom: PD001866; Calreticulin; 1.  
DR PROSITE: PS00804; CALRETICULIN\_2; 1.  
DR PROSITE: PS00805; CALRETICULIN\_REPEAT; 3.  
DR PROSITE: PS00014; ER\_TARGET; UNKNOWN\_1.  
FT NON\_TER 1  
SQ SEQUENCE 321 AA; 37367 MW; 6E8DFA98D42F7AEF CRC64;

Query Match 65.6%; Score 99; DB 13; Length 321;  
Best Local Similarity 66.7%; Pred. No. 3.3e-06;  
Matches 18; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY 1 CGPGTKKKVHVIVNYGKKNVLINKDIRC 27  
DB 36 CGYSTAKKVVHVLNSKGNHLIRKEVNC 62

Search completed: January 9, 2002, 15:03:28  
Job time: 270 sec

GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: January 9, 2002, 15:12:15 ; Search time 25.18 Seconds  
(without alignments)  
39.315 Million cell updates/sec

Title: US-09-828-000-5

Perfect score: 151

Sequence: 1 CGPCTKKVHVIFNYKGNVLINKDIRC 27

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 100059 seqs, 36664827 residues

Total number of hits satisfying chosen parameters: 100059

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt\_39:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	151	100.0	400	1 CRT1_BOVIN	P52193 bos taurus
2	151	100.0	416	1 CRTC_MOUSE	P14211 mus musculus
3	151	100.0	416	1 CRTC_RAT	P18418 rattus norv
4	151	100.0	417	1 CRTC_HUMAN	P27797 homo sapien
5	151	100.0	418	1 CRTC_RABIT	P15253 oryctolagus
6	151	100.0	421	1 CRT2_BOVIN	P42918 bos taurus
7	134	88.7	406	1 CRTC_DROME	P29413 drosophila
8	121	80.1	388	1 RAL1_ONCVO	P11012 onchocerca
9	112	74.2	393	1 CRTC_SCHMA	Q08814 schistosoma
10	97	64.2	420	1 CRTC_CHLRE	Q98td3 chlamydomon
11	96.5	63.9	395	1 CRTC_CAEEL	P27798 caenorhabdi
12	92	60.9	416	1 CRTC_BETVU	O81919 beta vulgar
13	88	58.3	424	1 CRT3_ARATH	O04153 arabidopsis
14	87	57.6	421	1 CRTC_PRUAR	O9xf98 prunus arne
15	87	57.6	424	1 CRT2_ARATH	Q38658 arabidopsis
16	83.5	55.3	424	1 CRTC_DICDI	Q23858 dictyosteli
17	83	55.0	424	1 CRTC_ORYSA	O9sly8 oryza sativ
18	83	55.0	425	1 CRT1_ARATH	O04151 arabidopsis
19	82.5	54.6	401	1 CRTC_EUGGR	O92ny3 euglena gra
20	82	54.3	415	1 CRTC_RICCO	P93508 ricinus com
21	76	50.3	416	1 CRTC_NICPL	Q40401 nicotiana p
22	71	47.0	420	1 CRTC_MAIZE	Q9sp22 zea mays (m
23	68	45.0	416	1 CRTC_BERST	Q9zpp1 berberis st
24	53	35.1	463	1 VDAH_CHICK	Q90578 gallus gall
25	52	34.4	1938	1 MYSD_CAEEL	P02567 caenorhabdi
26	51	33.8	560	1 YECO_YEAST	P39994 saccharomyc
27	51	33.8	725	1 NCA2_MOUSE	P13594 mus musculu
28	51	33.8	761	1 NCA2_HUMAN	P13592 homo sapien
29	51	33.8	848	1 NCA1_HUMAN	P13591 homo sapien
30	51	33.8	853	1 NCA1_BOVIN	P13836 bos taurus
31	51	33.8	858	1 NCA1_RAT	P13596 rattus norv
32	51	33.8	1091	1 NCA1_CHICK	P13590 gallus gall
33	51	33.8	1115	1 NCA1_MOUSE	P13595 mus musculu

Query Match 100.0%; Score 151; DB 1; Length 400;  
Best Local Similarity 100.0%; Pred. No. 2.4e-14;

## ALIGNMENTS

RESULT 1

ID	CRT1_BOVIN	STANDARD;	PRT;	400 AA.
AC	P52193;			
DT	01-OCT-1996 (Rel. 34, Created)			
DT	01-OCT-1996 (Rel. 34, Last sequence update)			
DT	01-OCT-1996 (Rel. 34, Last annotation update)			
DE	CALRETICULIN, BRAIN ISOFORM 1 (CRP55) (CALREGULIN) (HACBP).			
OS	Bos taurus (Bovine).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;			
OC	Bovidae; Bovinae; Bos.			
OX	NCBI_TaxID=9913;			
RN	[1]			
RP	SEQUENCE.			
RC	TISSUE=Brain;			
RX	MEDLINE=941183174; PubMed=8135753;			
RA	Matsuoka K., Seta K., Yamakawa Y., Okuyama T., Isobe T.;			
RT	*Covalent structure of bovine brain calreticulin.*;			
RL	Biochem. J. 298:435-442(1994).			
CC	!- FUNCTION: THIS PROTEIN BINDS CALCIUM. THERE ARE BOTH HIGH AND LOW AFFINITY CALCIUM-BINDING SITES.			
CC	!- SUBUNIT: MONOMER.			
CC	!- SUBCELLULAR LOCATION: ENDOPLASMIC RETICULUM LUMEN.			
CC	!- SIMILARITY: BELONGS TO THE CALRETICULIN FAMILY.			
DR	InterPro: IPR001580; Calreticulin.			
DR	InterPro: IPR000886; ER-target.			
DR	Pfam: PF00262; calreticulin; 1.			
DR	PRINTS: PR00626; CALRETICULIN.			
DR	ProDom: PD001866; Calreticulin; 1.			
DR	PROSITE: PS00014; ER-TARGET; 1.			
DR	PROSITE: PS00803; CALRETICULIN_1; 1.			
DR	PROSITE: PS00804; CALRETICULIN_2; 1.			
DR	PROSITE: PS00805; CALRETICULIN_REPEAT; 3.			
KW	Endoplasmic reticulum; Calcium-binding; Repeat; Glycoprotein.			
FT	DOMAIN 1 180 N-DOMAIN.			
FT	DOMAIN 181 291 P-DOMAIN.			
FT	DOMAIN 292 400 C-DOMAIN.			
FT	DOMAIN 174 238 4 X APPROXIMATE REPEATS.			
FT	REPEAT 174 185 1-1.			
FT	REPEAT 193 204 1-2.			
FT	REPEAT 210 221 1-3.			
FT	REPEAT 227 238 1-4.			
FT	DOMAIN 242 280 3 X APPROXIMATE REPEATS.			
FT	REPEAT 242 252 2-1.			
FT	REPEAT 256 266 2-2.			
FT	REPEAT 270 280 2-3.			
FT	DOMAIN 334 390 ASP/GLU/LYS-RICH.			
FT	DISULFID 120 146			
FT	CARBOHYD 162 162			
FT	SITE 397 400 N-LINKED (GLCNAC. . .).			
SQ	SEQUENCE 400 AA; 46381 MW; 7D4B68DFC689EEF1 CRC64;			

34	49	32.5	877	1	DPOL_BACCA	Q04957 bacillus ca
35	48.5	32.1	359	1	MLTA_BUCAL	P57531 buchnera ap
36	48.5	32.1	1766	1	RPB1_TRYBB	P17545 trypanosoma
37	48.5	32.1	1766	1	RPB2_TRYBB	P17546 trypanosoma
38	47.5	31.5	619	1	CALX_CAEEL	P34652 caenorhabdi
39	47	31.1	170	1	Y887_MYCTU	Q10548 mycobacteri
40	47	31.1	273	1	FPG_STRMU	P55045 streptococc
41	47	31.1	490	1	PURA_ARATH	Q96529 arabidopsis
42	47	31.1	1088	1	NCA1_XENLA	P16170 xenopus lae
43	47	31.1	1092	1	NCA2_XENLA	P36335 xenopus lae
44	46.5	30.8	334	1	CHI3_TOBAC	P29059 nicotiana t
45	46.5	30.8	551	1	CALX_PEA	O82709 pisum sativ

Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGPGTKKVVHVFYKGNVINKDIRC 27  
 |||||  
 DB 120 CGPGTKKVVHVFYKGNVINKDIRC 146

RESULT 2  
 CRTC\_MOUSE  
 ID CRTC\_MOUSE STANDARD; PRT; 416 AA.  
 AC P14211;  
 DT 01-JAN-1990 (Rel. 13, Created)  
 DT 01-JAN-1990 (Rel. 13, Last sequence update)  
 DT 15-DEC-1998 (Rel. 37, Last annotation update)  
 DE CALRETICULIN PRECURSOR (CRP55) (CALREGULIN) (HACBP) (ERP60).  
 GN CALR.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID:10090;  
 RN [1]  
 RN SEQUENCE FROM N.A., AND SEQUENCE OF 18-48 AND 129-161.  
 RP STRAIN=BALE/C; TISSUE=Liver;  
 RX MEDLINE=90059955; PubMed 2583110;  
 RA Smith M.J., Koch G.L.E.  
 RT "Multiple zones in the sequence of calreticulin (CRP55, calregulin,  
 RT HACBP), a major calcium binding ER/SR protein.";  
 RL EMBO J. 8:3581-3586(1989).  
 RN [2]  
 RN SEQUENCE FROM N.A.  
 RX MEDLINE=93013037; PubMed 1398135;  
 RA Mazzarella R.A., Gold P., Cunningham M., Green M.;  
 RT "Determination of the sequence of an expressible cDNA clone encoding  
 RT Fkp60/calregulin by the use of a novel nested set method.";  
 RL Gene 120:217-225(1992).  
 RN [3]  
 RN SEQUENCE OF 18-38.  
 RP TISSUE=Fibroblast;  
 RX MEDLINE=95009907; PubMed 7523108;  
 RA Merrick B.A., Patterson R.M., Wichter L.L., He C., Selkirk J.K.;  
 RT "Separation and sequencing of familial and novel murine proteins  
 RT using preparative two-dimensional gel electrophoresis.";  
 RL Electrophoresis 15:735-745(1994).  
 CC -1- FUNCTION: THIS PROTEIN BINDS CALCIUM. THERE ARE BOTH HIGH AND  
 CC LOW AFFINITY CALCIUM-BINDING SITES.  
 CC -1- SUBUNIT: MONOMER (BY SIMILARITY).  
 CC -1- SUBCELLULAR LOCATION: ENDOPLASMIC RETICULUM LUMEN.  
 CC -1- SIMILARITY: BELONGS TO THE CALRETICULIN FAMILY.  
 CC -----  
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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 DR EMBL: X14926; CAA33053.1; -.  
 DR MBL: M92988; AAA37569.1; -.  
 DR PIR: S06763; S06763.  
 DR JGI: JGI1444; JGI1444.  
 DR SWISS-2DPAGE: P14211; MOUSE.  
 DR MGI: MGI:88252; Calr.  
 DR InterPro: IPR001580; Calreticulin.  
 DR InterPro: IPR000886; ER\_target.  
 DR Pfam: PF00262; calreticulin; 1.  
 DR PRINTS: PR00626; CALRETICULIN.  
 DR ProDom: PD001866; Calreticulin; 1.  
 DR PROSITE: PS00014; ER\_TARGET; 1.  
 DR PROSITE: PS00803; CALRETICULIN\_1; 1.  
 DR PROSITE: PS00804; CALRETICULIN\_2; 1.  
 DR PROSITE: PS00805; CALRETICULIN\_REPEAT; 3.  
 KW Endoplasmic reticulum; Calcium-binding; Repeat; Signal.

FT SIGNAL 1 17  
 FT CHAIN 18 416  
 FT DOMAIN 18 197  
 FT DOMAIN 198 308  
 FT DOMAIN 309 416  
 FT DOMAIN 191 255  
 FT REPEAT 191 202  
 FT REPEAT 210 221  
 FT REPEAT 227 238  
 FT REPEAT 244 255  
 FT DOMAIN 259 297  
 FT REPEAT 259 269  
 FT REPEAT 273 283  
 FT REPEAT 287 297  
 FT DOMAIN 351 407  
 FT DISULFID 137 163  
 FT SITE 413 416  
 SQ SEQUENCE 416 AA; 47994 MW; 24C03B00913408D8 CRC64;

Query Match 100.0%; Score 151; DB 1; Length 416;  
 Best Local Similarity 100.0%; Pred. No. 2.5e-14;  
 Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGPGTKKVVHVFYKGNVINKDIRC 27  
 |||||  
 DB 137 CGPGTKKVVHVFYKGNVINKDIRC 163

RESULT 3  
 CRTC\_RAT  
 ID CRTC\_RAT STANDARD; PRT; 416 AA.  
 AC P18418; P10452;  
 DT 01-MAR-1989 (Rel. 10, Created)  
 DT 01-NOV-1990 (Rel. 16, Last sequence update)  
 DT 01-NOV-1997 (Rel. 35, Last annotation update)  
 DE CALRETICULIN PRECURSOR (CRP55) (CALREGULIN) (HACBP) (ERP60) (CALBP)  
 DE (CALCIUM-BINDING PROTEIN 3) (CABP3).  
 GN CALR.  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 OX NCBI\_TaxID:10116;  
 RN [1]  
 RN SEQUENCE FROM N.A.  
 RP STRAIN=SPRAGUE-DAWLEY; TISSUE=Brain cortex;  
 RX MEDLINE=90370496; PubMed=2395661;  
 RA Murthy K.K., Banville D., Srikant C.B., Carrier F., Bell A.,  
 RA Holmes C., Patel V.C.;  
 RT "Structural homology between the rat calreticulin gene product and  
 RT the Onchocerca volvulus antigen Ral-1.";  
 RL Nucleic Acids Res. 18:4933-4933(1990).  
 RN [2]  
 RN SEQUENCE FROM N.A.  
 RP STRAIN=SPRAGUE-DAWLEY;  
 RX MEDLINE=93202172; PubMed=8453984;  
 RA Nakamura M., Moriya M., Baba T., Michikawa Y., Yamanobe T., Arai K.,  
 RA Okinaga S., Kobayashi T.;  
 RT "An endoplasmic reticulum protein, calreticulin, is transported into  
 RT the acrosome of rat sperm.";  
 RL Exp. Cell Res. 205:101-110(1993).  
 RN [3]  
 RN SEQUENCE FROM N.A.  
 RP STRAIN=SPRAGUE-DAWLEY;  
 RX MEDLINE=95181573; PubMed=7876339;  
 RA Soenichsen B., Fuellekrug J., van Nguyen P., Diekmann W.,  
 RA Robinson D.G., Mieskes G.;  
 RT "Retention and retrieval: both mechanisms cooperate to maintain  
 RT calreticulin in the endoplasmic reticulum.";  
 RL J. Cell Sci. 107:2705-2717(1994).  
 RN [4]  
 RN SEQUENCE OF 270-358 FROM N.A.  
 RP STRAIN=SPRAGUE-DAWLEY;

RA Lone Y.C., Bailly A., Latruffe N.;  
 RN Submitted (DEC-1988) to the EMBL/GenBank/DBJ databases.  
 RL [5]  
 RP SEQUENCE OF 18-29.  
 RX MEDLINE=91054414; PubMed=2241926;  
 RA Treves S., de Mattei M., Lanfredi M., Villa A., Green N.M.,  
 RA MacLennan D.H., Meldolesi J., Pozzan T.;  
 RT "Calreticulin is a candidate for a calsequestrin-like function in  
 RT Ca2(+)-storage compartments (calcosomes) of liver and brain.";  
 RL Biochem. J. 271:473-480(1990).  
 RN [6]  
 RP SEQUENCE OF 18-32.  
 RC STRAIN=SPRAGUE-DAWLEY; TISSUE=Testis;  
 RX MEDLINE=92360010; PubMed=1497655;  
 RA Nakamura M., Michikawa Y., Baba T., Okinaga S., Arai K.;  
 RT "Calreticulin is present in the acrosome of spermatids of rat  
 RT testis.";  
 RL Biochem. Biophys. Res. Commun. 186:668-673(1992).  
 RN [7]  
 RP SEQUENCE OF 18-32.  
 RC STRAIN=LEC; TISSUE=Liver;  
 RX MEDLINE=94072621; PubMed=8251535;  
 RA Yokoi T., Nagayama S., Kajiwara R., Kawaguchi Y., Horiuchi R.,  
 RA Kametaki T.;  
 RT "Identification of protein disulfide isomerase and calreticulin as  
 RT autoimmune antigens in LEC strain of rats.";  
 RL Biochim. Biophys. Acta 1158:339-344(1993).  
 CC -!- FUNCTION: THIS PROTEIN BINDS CALCIUM. THERE ARE BOTH HIGH AND  
 CC LOW AFFINITY CALCIUM-BINDING SITES.  
 CC -!- SUBUNIT: MONOMER (BY SIMILARITY).  
 CC -!- SUBCELLULAR LOCATION: ENDOPLASMIC RETICULUM LUMEN.  
 CC -!- SIMILARITY: BELONGS TO THE CALRETICULIN FAMILY.  
 CC -!- CAUTION: WAS ORIGINALLY (REF.2) THOUGHT TO BE D-BETA-  
 CC HYDROXYBUTYRATE DEHYDROGENASE.  
 CC -----  
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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 DR EMBL: D78308; BA011345.1; -  
 DR EMBL: X53363; CAA37446.1; -  
 DR EMBL: X13702; CAA31987.1; ALT\_SEQ.  
 DR EMBL: X79327; CAA55890.1; -  
 DR PIR: S04867; S04867.  
 DR PIR: S11205; S11205.  
 DR PIR: S13045; S13045.  
 DR PIR: A49176; A49176.  
 DR PIR: S45036; S45036.  
 DR PIR: JH0819; JH0819.  
 DR InterPro: IPR001580; Calreticulin.  
 DR InterPro: IPR000886; ER.target.  
 DR Pfam: PF00262; calreticulin; 1.  
 DR PRINTS: PR00626; CALRETICULIN.  
 DR PRODOM: PD001866; Calreticulin; 1.  
 DR PROSITE: PS00014; ER-TARGET; 1.  
 DR PROSITE: PS00803; CALRETICULIN\_1; 1.  
 DR PROSITE: PS00804; CALRETICULIN\_2; 1.  
 DR PROSITE: PS00805; CALRETICULIN\_REPEAT; 3.  
 KW Endoplasmic reticulum; Calcium-binding; Repeat; Signal.  
 FT SIGNAL 1 17  
 FT CHAIN 18 416 CALRETICULIN.  
 FT DOMAIN 18 197 N-DOMAIN.  
 FT DOMAIN 198 308 P-DOMAIN.  
 FT DOMAIN 309 416 C-DOMAIN.  
 FT DOMAIN 191 255 4 X APPROXIMATE REPEATS.  
 FT REPEAT 191 202 1-1.  
 FT REPEAT 202 221 1-2.  
 FT REPEAT 221 238 1-3.  
 FT REPEAT 238 255 1-4.

FT DOMAIN 259 297 3 X APPROXIMATE REPEATS.  
 FT REPEAT 259 269 2-1.  
 FT REPEAT 273 283 2-2.  
 FT REPEAT 287 297 2-3.  
 FT DOMAIN 351 407 ASP/GLU/LYS-RICH.  
 FT DISULFID 137 163 BY SIMILARITY.  
 FT SITE 413 416 PREVENT SECRETION FROM ER.  
 SQ SEQUENCE. 416 AA; 47995 MW; 2E6713CED31A2970 CRC64;  
 Query Match 100.0%; Score 151; DB 1; Length 416;  
 Best Local Similarity 100.0%; Pred. No. 2.5e-14;  
 Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 CGPGTKKHVIFNYKGNVINKDIRC 27  
 Db 137 CGPGTKKHVIFNYKGNVINKDIRC 163  
 RESULT 4  
 CRTC\_HUMAN  
 ID CRTC\_HUMAN STANDARD; PRT: 417 AA.  
 AC P27797;  
 DT 01-AUG-1992 (Rel. 23, Created)  
 DT 01-AUG-1992 (Rel. 23, Last sequence update)  
 DT 20-AUG-2001 (Rel. 40, Last annotation update)  
 DE CALRETICULIN PRECURSOR (CRP55) (CALREGULIN) (HACBP) (ERP60) (52 KDA  
 DE RIBONUCLEOPROTEIN AUTOANTIGEN RO/SS-A).  
 GN CALR OR CRTC.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=92013129; PubMed=1919005;  
 RA Rokeach L.A., Haselby J.A., Melloy J.F., Smeenk R.J., Unnasch T.R.,  
 RA Greene B.M., Hoch S.O.;  
 RT "Characterization of the autoantigen calreticulin.";  
 RL J. Immunol. 147:3031-3039(1991).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=90237213; PubMed=2332496;  
 RA McCaulliffe D.P., Lux F.A., Lieu T.S., Sanz I., Hanke J., Newkirk M.M.,  
 RA Bachinski L.L., Itoh Y., Siciliano M.J., Reichlin M., Sontheimer R.D.,  
 RA Capra J.D.;  
 RT "Molecular cloning, expression, and chromosome 19 localization of a  
 RT human Ro/SS-A autoantigen.";  
 RL J. Clin. Invest. 85:1379-1391(1990).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=92129342; PubMed=1733953;  
 RA McCaulliffe D.P., Yang Y.S., Wilson J., Sontheimer R.D., Capra J.D.;  
 RT "The 5'-flanking region of the human calreticulin gene shares  
 RT homology with the human GRP78, GRP94, and protein disulfide isomerase  
 RT promoters.";  
 RL J. Biol. Chem. 267:2557-2562(1992).  
 RN [4]  
 RP SEQUENCE FROM N.A.  
 RA Lamerding J., McCreedy P., Stilwagen S., Ramirez M., Carrano A.;  
 RL Submitted (MAR-1997) to the EMBL/GenBank/DBJ databases.  
 RN [5]  
 RP SEQUENCE OF 18-36.  
 RX MEDLINE=92002034; PubMed=1911778;  
 RA Rojiani M.V., Finlay B.B., Gray V., Dedhar S.;  
 RT "In vitro interaction of a polypeptide homologous to human Ro/SS-A  
 RT antigen (calreticulin) with a highly conserved amino acid sequence in  
 RT the cytoplasmic domain of integrin alpha subunits.";  
 RL Biochemistry 30:9859-9866(1991).  
 RN [6]  
 RP SEQUENCE OF 18-32.  
 RX MEDLINE=90380058; PubMed=2400400;  
 RA Krause K.H., Simmerman H.K.B., Jones L.R., Campbell K.P.;

\*Sequence similarity of calreticulin with a Ca2(+)-binding protein that co-purifies with an Ins(1,4,5)P3-sensitive Ca2+ store in HL-60 cells.\*;  
 Biochem. J. 270:545-548(1990).  
 [7]

SEQUENCE OF 18-28.  
 RC TISSUE Liver;  
 RX MEDLINE 93162045; PubMed 1286669;  
 RA Hochstrasser D.F., Frutiger S., Paquet N., Bairoch A., Ravier F.,  
 RA Pasquali C., Sanchez J.-C., Tissot J.-D., Bjellqvist B., Vargas R.,  
 RA Appel R.D., Hughes G.J.;  
 RT \*Human liver protein map: a reference database established by  
 RT microsequencing and gel comparison.\*;  
 RL Electrophoresis 13:992-1001(1992).  
 [8]

PARTIAL SEQUENCE OF 25-34; 56-62; 208-221 AND 273-278.  
 RC TISSUE Keratinocytes;  
 RX MEDLINE 93162043; PubMed 1286667;  
 RA Rasmussen H.H., van Damme J., Puype M., Gesser B., Celis J.E.,  
 RA Vandekerckhove J.;  
 RT \*Microsequences of 145 proteins recorded in the two-dimensional gel  
 RT protein database of normal human epidermal keratinocytes.\*;  
 RL Electrophoresis 13:960-969(1992).  
 [9]

SEQUENCE OF 18-26.  
 RC TISSUE Colon carcinoma;  
 RX MEDLINE 97295306; PubMed 9150948;  
 RA Ji H., Reid G.E., Moritz R.L., Eddes J.S., Burgess A.W., Simpson R.J.;  
 RA \*A two-dimensional gel database of human colon carcinoma proteins.\*;  
 RL Electrophoresis 18:605-613(1997).  
 CC -!- FUNCTION: THIS PROTEIN BINDS CALCIUM. THERE ARE BOTH HIGH AND  
 CC LOW AFFINITY CALCIUM-BINDING SITES.

-!- SUBUNIT: MONOMER (BY SIMILARITY)  
 CC -!- SUBCELLULAR LOCATION: ENDOPLASMIC RETICULUM LUMEN.  
 CC -!- SIMILARITY: BELONGS TO THE CALRETICULIN FAMILY.  
 CC -!- CAUTION: WAS ORIGINALLY (REF.2) THOUGHT TO BE THE RO AUTOANTIGEN.

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EMBL; H84739; AAA51916.1; -;  
 EMBL; M12294; AAA76582.1; -;  
 EMBL; AD000092; BAB51176.1; -;  
 PIR; A37047; A37047.  
 PIR; S11475; S11475.  
 PIR; A42330; A42330.  
 PIR; A46452; A46452.  
 SWISS-2DPAGE; P27797; HUMAN.  
 Aarhus/Ghent-2DPAGE; 9401; IEF.  
 HSC-2DPAGE; P27797; HUMAN.  
 MIM; 109091; -;  
 InterPro; IPR001580; Calreticulin.  
 InterPro; IPR000886; ER-target.  
 Pfam; PF00462; calreticulin; 1.  
 PRINTS; P00626; CALRETICULIN.  
 ProDom; PD001866; Calreticulin; 1.  
 PROSITE; PS00014; ER-TARGET; 1.  
 PROSITE; PS00803; CALRETICULIN; 1.  
 PROSITE; PS00804; CALRETICULIN; 2; 1.  
 PROSITE; PS00805; CALRETICULIN-REPEAT; 3.  
 Endoplasmic reticulum; Calcium-binding; Repeat; Signal.  
 SIGNAL 1 17  
 CHAIN 18 417 CALRETICULIN.  
 FT CHAIN 18 197 N-DOMAIN.  
 FT DOMAIN 188 308 P-DOMAIN.  
 FT DOMAIN 309 417 C-DOMAIN.  
 FT DOMAIN 191 255 4 X APPROXIMATE REPEATS.  
 FT REPEAT 191 202 1-1.

FT REPEAT 210 221 1-2.  
 FT REPEAT 227 238 1-3.  
 FT REPEAT 244 255 1-4.  
 FT DOMAIN 259 297 3 X APPROXIMATE REPEATS.  
 FT REPEAT 269 297 2-1.  
 FT REPEAT 273 283 2-2.  
 FT REPEAT 287 297 2-3.  
 FT DOMAIN 351 408 ASP/GLU/LYS-RICH.  
 FT DISULFID 137 163 BY SIMILARITY.  
 FT SITE 414 417 PREVENT SECRETION FROM ER.  
 FT CONFLICT 35 35 MISSING (IN REF. 3).  
 SQ SEQUENCE 417 AA; 48141 MW; BC37C3C0F1054FB2 CRC64;  
 Query Match 100.0%; Score 151; DB 1; Length 417;  
 Best local Similarity 100.0%; Pred. No. 2.5e-14;  
 Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 CGPGTKKHVHVIENYKGNVINKDIRC 27  
 Db 137 CGPGTKKHVHVIENYKGNVINKDIRC 163  
 RESULT 5  
 ID CRTCL\_RABIT STANDARD; PRT; 418 AA.  
 AC P15253;  
 DT 01-APR-1990 (Rel. 14, Created)  
 DT 01-APR-1990 (Rel. 14, Last sequence update)  
 DT 01-OCT-1996 (Rel. 34, Last annotation update)  
 DE CALRETICULIN PRECURSOR (CRP55) (CALREGULIN) (HACBP) (ERP60).  
 GN CALR.  
 OS Oryctolagus cuniculus (Rabbit).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.  
 OX NCBI\_TaxID:9986;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE:Slow-twitch skeletal muscle;  
 RX MEDLINE 90094320; PubMed-2600080;  
 RA Fliegel L., Burns K., MacLennan D.H., Reithmeier R.A.F., Michalak M.;  
 RT \*Molecular cloning of the high affinity calcium-binding protein  
 RT (calreticulin) of skeletal muscle sarcoplasmic reticulum.\*;  
 RL J. Biol. Chem. 264:21522-21528(1989).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE:Fast-twitch skeletal muscle;  
 RX MEDLINE 91282795; PubMed-2059224;  
 RA Fliegel L., Michalak M.;  
 RT \*Fast-twitch and slow-twitch skeletal muscles express the same  
 RT isoform of calreticulin.\*;  
 RL Biochem. Biophys. Res. Commun. 177:979-984(1991).  
 RN [3]  
 RP SEQUENCE OF 18-36.  
 RX MEDLINE 91054414; PubMed-2241926;  
 RA Treves S., de Mattei M., Lanfredi M., Villa A., Green N.M.,  
 RA MacLennan D.H., Meldolesi J., Pozzan T.;  
 RT \*Calreticulin is a candidate for a calsequestrin-like function in  
 RT Ca2(+)-storage compartments (calcosomes) of liver and brain.\*;  
 RL Biochem. J. 271:473-480(1990).  
 RN [4]  
 RP SEQUENCE OF 18-46.  
 RX MEDLINE 91201375; PubMed-2016321;  
 RA Milner R.E., Baksh S., Shemanko C., Carpenter M.R., Smillie L.,  
 RA Vance J.E., Opas M., Michalak M.;  
 RT \*Calreticulin, and not calsequestrin, is the major calcium binding  
 RT protein of smooth muscle sarcoplasmic reticulum and liver endoplasmic  
 RT reticulum.\*;  
 RL J. Biol. Chem. 266:7155-7165(1991).  
 RN [5]  
 RP PARTIAL SEQUENCE.  
 RT TISSUE Lung;  
 RX MEDLINE 92002038; PubMed-1911780;

RA Guan S., Fallick A.M., Williams D.E., Cashman J.R.;  
 RT "Evidence for complex formation between rabbit lung flavin-containing  
 RL monooxygenase and calreticulin.";  
 CC Biochemistry 30:9892-9900(1991).  
 CC -!- FUNCTION: THIS PROTEIN BINDS CALCIUM. THERE ARE BOTH HIGH AND  
 CC LOW AFFINITY CALCIUM-BINDING SITES.  
 CC -!- SUBUNIT: MONOMER (BY SIMILARITY).  
 CC -!- SUBCELLULAR LOCATION: ENDOPLASMIC RETICULUM LUMEN.  
 CC -!- SIMILARITY: BELONGS TO THE CALRETICULIN FAMILY.  
 CC -----  
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 CC -----  
 DR EMBL: J05138; AAA31188.1; -;  
 DR PIR: A34154; A34154.  
 DR PIR: C33208; C33208.  
 DR PIR: D33208; D33208.  
 DR PIR: E33208; E33208.  
 DR PIR: F33208; F33208.  
 DR PIR: S13046; S13046.  
 DR PIR: S13047; S13047.  
 DR InterPro: IPR001580; Calreticulin.  
 DR InterPro: IPR000886; ER target.  
 DR Pfam: PF00262; calreticulin; 1.  
 DR PRINTS: PR00626; CALRETICULIN.  
 DR PRODOM: PD001866; Calreticulin; 1.  
 DR PROSITE: PS00014; ER\_TARGET; 1.  
 DR PROSITE: PS00803; CALRETICULIN\_1; 1.  
 DR PROSITE: PS00804; CALRETICULIN\_2; 1.  
 DR PROSITE: PS00805; CALRETICULIN\_REPEAT; 3.  
 KW Endoplasmic reticulum; Calcium-binding; Repeat; Signal.  
 FT SIGNAL 1 17  
 FT CHAIN 18 418 CALRETICULIN.  
 FT DOMAIN 18 197 N-DOMAIN.  
 FT DOMAIN 198 308 P-DOMAIN.  
 FT DOMAIN 309 418 C-DOMAIN.  
 FT DOMAIN 191 255 4 X APPROXIMATE REPEATS.  
 FT REPEAT 191 202 1-1.  
 FT REPEAT 210 221 1-2.  
 FT REPEAT 227 238 1-3.  
 FT REPEAT 244 255 1-4.  
 FT DOMAIN 259 297 3 X APPROXIMATE REPEATS.  
 FT REPEAT 259 269 2-1.  
 FT REPEAT 273 283 2-2.  
 FT REPEAT 287 297 2-3.  
 FT DOMAIN 351 408 ASP/GLU/LYS-RICH.  
 FT DISULFID 137 163 BY SIMILARITY.  
 FT SITE 415 418 PREVENT SECRETION FROM ER.  
 FT VARIANT 35 35 E -> D.  
 FT CONFLICT 90 90 P -> T (IN REF. 5).  
 SQ SEQUENCE 418 AA; 48275 MW; B6082B689DC763A6 CRC64;

Query Match 100.0%; Score 151; DB 1; Length 418;  
 Best Local Similarity 100.0%; Pred. No. 2.6e-14;  
 Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 CGPGTKKVVHVFNYKGNVINKNDIRC 27  
 |||||  
 Db 137 CGPGTKKVVHVFNYKGNVINKNDIRC 163

RESULT 6  
 ID CRT2\_BOVIN STANDARD; PRT; 421 AA.  
 AC P42918;  
 DT 01-NOV-1995 (Rel. 32, Created)  
 DT 01-NOV-1995 (Rel. 32, Last sequence update)

DT 15-JUL-1998 (Rel. 36, Last annotation update)  
 DE CALRETICULIN, BRAIN ISOFORM 2 PRECURSOR (CRP55) (CALREGULIN) (HACBP).  
 OS Bos taurus (Bovine).  
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
 CC Bovidae; Bovinae; Bos.  
 CC NCBI\_taxid=9913;  
 RN [1]  
 RC SEQUENCE FROM N.A.  
 RC TISSUE=Brain;  
 RX MEDLINE=93385184; PubMed=8373827;  
 RA Liu N., Fine R.E., Johnson R.J.;  
 RT "Comparison of cDNAs from bovine brain coding for two isoforms of  
 RL calreticulin.";  
 RL Biochim. Biophys. Acta 1202:70-76(1993).  
 CC -!- FUNCTION: THIS PROTEIN BINDS CALCIUM. THERE ARE BOTH HIGH AND  
 CC LOW AFFINITY CALCIUM-BINDING SITES.  
 CC -!- SUBUNIT: MONOMER (BY SIMILARITY).  
 CC -!- SUBCELLULAR LOCATION: ENDOPLASMIC RETICULUM LUMEN.  
 CC -!- SIMILARITY: BELONGS TO THE CALRETICULIN FAMILY.  
 CC -----  
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 CC -----  
 DR EMBL: L13462; AAC37307.1; -;  
 DR InterPro: IPR001580; Calreticulin.  
 DR InterPro: IPR000886; ER target.  
 DR Pfam: PF00262; calreticulin; 1.  
 DR PRINTS: PR00626; CALRETICULIN.  
 DR PRODOM: PD001866; Calreticulin; 1.  
 DR PROSITE: PS00014; ER\_TARGET; 1.  
 DR PROSITE: PS00803; CALRETICULIN\_1; 1.  
 DR PROSITE: PS00804; CALRETICULIN\_2; 1.  
 DR PROSITE: PS00805; CALRETICULIN\_REPEAT; 3.  
 KW Endoplasmic reticulum; Calcium-binding; Repeat; Signal.  
 FT SIGNAL 1 34 POTENTIAL.  
 FT CHAIN 35 421 CALRETICULIN, BRAIN ISOFORM 2.  
 FT DOMAIN 35 201 N-DOMAIN.  
 FT DOMAIN 202 312 P-DOMAIN.  
 FT DOMAIN 313 421 C-DOMAIN.  
 FT DOMAIN 195 259 4 X APPROXIMATE REPEATS.  
 FT REPEAT 195 206 1-1.  
 FT REPEAT 214 225 1-2.  
 FT REPEAT 231 242 1-3.  
 FT REPEAT 248 259 1-4.  
 FT REPEAT 263 301 3 X APPROXIMATE REPEATS.  
 FT REPEAT 263 273 2-1.  
 FT REPEAT 277 287 2-2.  
 FT REPEAT 291 301 2-3.  
 FT DOMAIN 366 411 ASP/GLU/LYS-RICH.  
 FT DISULFID 141 167 BY SIMILARITY.  
 FT CARBOHYD 183 183 N-LINKED (GLCNAC. .) (POTENTIAL).  
 FT SITE 418 421 PREVENT SECRETION FROM ER.  
 SQ SEQUENCE 421 AA; 48812 MW; 0257E959F71528BC CRC64;

Query Match 100.0%; Score 151; DB 1; Length 421;  
 Best Local Similarity 100.0%; Pred. No. 2.6e-14;  
 Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 CGPGTKKVVHVFNYKGNVINKNDIRC 27  
 |||||  
 Db 141 CGPGTKKVVHVFNYKGNVINKNDIRC 167

RESULT 7  
 ID CRTC\_DROME STANDARD; PRT; 406 AA.

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AC P29413; Q9VHA3;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-OCT-1993 (Rel. 27, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE CALRETICULIN PRECURSOR (CRP55) (CALREGULIN) (HACBP).
GN CRC OR CG9429.
OS Drosophila melanogaster (Fruit fly).
OC Pterygota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Eukaryota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID 7227;
KN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE 93208374; PubMed 1296819;
RA Smith M.J.;
RT "Nucleotide sequence of a Drosophila melanogaster gene encoding a
KL calreticulin homologue.";
RN DNA Seq. 3:247-250(1992).
RP [2]
RP SEQUENCE FROM N.A.
RX STRAIN-BERKELEY;
RX MEDLINE-20196006; PubMed-10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amaratides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galie R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Vandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Abuyani A., An H.-J., Andrews-Frannkoch C., Baldwin D.,
RA Ballwe R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berlan B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Hurlis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablo B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Fostler C., Gabrielian A.E., Garq N.S., Gelbart W.M., Glasser K.,
RA Glodok A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Laske P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattel B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Klanos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wasserman D.A., Weinstock G.M., Weissbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster.";
RL Science 287:2185-2195(2000).
RN [3]
RP SEQUENCE OF 91-124 AND 182-220.
RX MEDLINE 90307981; PubMed 2365822;
RA McCaulliffe D.P., Zappi E., Lieu T.S., Michalak M., Sontheimer R.D.,
RA Cupra J.D.;
RT "A human Ro/SS-A autoantigen is the homologue of calreticulin and is
KT highly homologous with onchocercal RAL-1 antigen and an aplysia
KT 'memory molecule'.";
RL J. Clin. Invest. 86:332-335(1990).
CC -!- FUNCTION: THIS PROTEIN BINDS CALCIUM. THERE ARE BOTH HIGH AND
CC LOW AFFINITY CALCIUM-BINDING SITES.
CC -!- SUBCELLULAR LOCATION: ENDOPLASMIC RETICULUM LUMEN.
CC -!- SIMILARITY: BELONGS TO THE CALRETICULIN FAMILY.

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CC -----
CC EMBL; X64461; CAA45791.1; -.
CC DR EMBL; AE003683; AAF54416.1; -.
CC DR PIR; A37158; A37158.
CC DR FlyBase; FBgn0005585; Crc.
CC DR InterPro; IPR001580; Calreticulin.
CC DR InterPro; IPR000886; ER_target.
CC DR Pfam; PF00262; calreticulin; 1.
CC DR PRINTS; PR00626; Calreticulin.
CC DR ProDom; PD001866; Calreticulin; 1.
CC DR PROSITE; PS00014; ER_TARGET; 1.
CC DR PROSITE; PS00803; CALRETICULIN_1; 1.
CC DR PROSITE; PS00804; CALRETICULIN_2; 1.
CC DR PROSITE; PS00805; CALRETICULIN_REPEAT; 3.
CC KW Endoplasmic reticulum; Calcium-binding; Repeat; Signal.
CC FT SIGNAL 1 17 POTENTIAL.
CC FT CHAIN 18 406 CALRETICULIN.
CC FT CONFLICT 107 107 G -> A (IN REF. 3).
CC FT CONFLICT 184 184 V -> L (IN REF. 3).
CC SQ SEQUENCE 406 AA; 46808 MW; 65D72C69D0BEC427 CRC64;
Query Match 88.7%; Score 134; DB 1; Length 406;
Best Local Similarity 88.9%; Pred. No. 6,7e-12;
Matches 24; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
QY 1 CGPGTKKHVHVFNYKGNVLNKDIRC 27
DB 137 CGPGTKKHVHVFNYKGNHLISKDIRC 163
RESULT 8
RAL1_ONCVO STANDARD; PRT; 388 AA.
AC P11012;
DT 01-JUL-1989 (Rel. 11, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE RAL-1 PROTEIN PRECURSOR (41 KDA LARVAL ANTIGEN).
GN RAL1.
OS Onchocerca volvulus.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Spirurida; Filarioidea;
OC Onchocercidae; Onchocerca.
OX NCBI_TaxID-6282;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-94341871; PubMed-7520419;
RA Rokeach L.A., Zimmerman P.A., Unnasch T.R.;
RT "Epitopes of the Onchocerca volvulus RAL1 antigen, a member of the
RT calreticulin family of proteins, recognized by sera from patients
RT with onchocerciasis.";
RL Infect. Immun. 62:3696-3704(1994).
RN [2]
RP SEQUENCE OF 53-388 FROM N.A.
RX MEDLINE-88273584; PubMed 2455736;
RA Unnasch T.R., Gallin M.Y., Soboslay P.T., Erttmann K.D., Greene B.M.;
RT "Isolation and characterization of expression cDNA clones encoding
RT antigens of Onchocerca volvulus infective larvae.";
RL J. Clin. Invest. 82:262-269(1988).
CC -!- SIMILARITY: BELONGS TO THE CALRETICULIN FAMILY.
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DR EMBL; M20565; AAA59056.1; -  
 DR PIR; A32507; A32507; Calreticulin.  
 DR InterPro; IPR001580; Calreticulin.  
 DR Pfam; PF00262; calreticulin; 1.  
 DR PRINTS; PR00626; CALRETICULIN.  
 DR PRODOM; PD001866; Calreticulin; 1.  
 DR PROSITE; PS00803; CALRETICULIN\_1; 1.  
 DR PROSITE; PS00804; CALRETICULIN\_2; 1.  
 DR PROSITE; PS00805; CALRETICULIN\_REPEAT; 3.  
 KW Calcium-binding; Repeat; Antigen; Signal;  
 FT SIGNAL 1 17 POTENTIAL.  
 FT CHAIN 18 388 RAL-1 PROTEIN.  
 FT DOMAIN 189 253 4 X APPROXIMATE REPEATS.  
 FT REPEAT 189 200 1-1.  
 FT REPEAT 208 219 1-2.  
 FT REPEAT 225 236 1-3.  
 FT REPEAT 242 253 1-4.  
 FT DOMAIN 257 295 3 X APPROXIMATE REPEATS.  
 FT REPEAT 257 267 2-1.  
 FT REPEAT 271 281 2-2.  
 FT REPEAT 285 295 2-3.  
 FT DOMAIN 353 388 ARG/LYS-RICH (BASIC).  
 FT DISULFID 135 161 BY SIMILARITY.  
 SQ SEQUENCE 388 AA; 45298 MW; 9537F298A2D31CD6 CRC64;

Query Match 80.1%; Score 121; DB 1; Length 388;  
 Best Local Similarity 77.8%; Pred. No. 4.7e-10;  
 Matches 21; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

OY 1 CGPGTKKHVIFNYKGNVLINKDIRC 27  
 |||||  
 DB 135 CGPGTKKHVIFNYKGNVLINKDIRC 161

## RESULT 9

CRTC\_SCHMA  
 ID CRTC\_SCHMA STANDARD; PRT; 393 AA.  
 AC Q08614; Q26562;  
 DT 01-JUN-1994 (Rel. 29, Created)  
 DT 01-FEB-1996 (Rel. 33, Last sequence update)  
 DT 01-NOV-1997 (Rel. 35, Last annotation update)  
 DE CALRETICULIN PRECURSOR (SMA PROTEIN).  
 OS Schistosoma mansoni (Blood fluke).  
 OC Eukaryota; Metazoa; Platyhelminthes; Turbellarian Platyhelminths;  
 OC Rhabditophora; Eulecithophora; Revertospermata; Mediofusata;  
 OC Neodermata; Trematoda; Digenea; Strigeldida; Schistosomatoidea;  
 OC Schistosomatidae; Schistosoma.  
 OX NCBI\_TaxID=6183;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=PUERTO RICAN;  
 RX MEDLINE=93165070; PubMed=8433712;  
 RA Khalife J., Trottein F., Schacht A.-M., Godin C., Pierce R.J.,  
 RA Capron A.;  
 RT "Cloning of the gene encoding a Schistosoma mansoni antigen  
 RT homologous to human Ro/SS-A autoantigen."  
 RL Mol. Biochem. Parasitol. 57:193-202(1993).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=PUERTO RICAN;  
 RX MEDLINE=94187805; PubMed=8139623;  
 RA Khalife J., Pierce R.J., Godin C., Capron A.;  
 RT "Cloning and sequencing of the gene encoding Schistosoma mansoni  
 RT calreticulin."  
 RL Mol. Biochem. Parasitol. 62:313-315(1993).  
 CC -!- FUNCTION: THIS PROTEIN BINDS CALCIUM. THERE ARE BOTH HIGH AND  
 CC LOW AFFINITY CALCIUM-BINDING SITES.  
 CC -!- SUBCELLULAR LOCATION: ENDOPLASMIC RETICULUM LUMEN.

CC -!- SIMILARITY: BELONGS TO THE CALRETICULIN FAMILY.  
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DR EMBL; M93097; AAA29854.1; -  
 DR EMBL; L24159; AAA19024.1; -  
 DR HSP; P00268; ARXN.  
 DR InterPro; IPR001580; Calreticulin.  
 DR Pfam; PF00262; calreticulin; 1.  
 DR PRINTS; PR00626; CALRETICULIN.  
 DR PRODOM; PD001866; Calreticulin; 1.  
 DR PROSITE; PS00014; ER-TARGET; 1.  
 DR PROSITE; PS00803; CALRETICULIN\_1; 1.  
 DR PROSITE; PS00804; CALRETICULIN\_2; 1.  
 DR PROSITE; PS00805; CALRETICULIN\_REPEAT; 1.  
 KW Endoplasmic reticulum; Calcium-binding; Repeat; Signal; Glycoprotein.  
 FT SIGNAL 1 16 POTENTIAL.  
 FT CHAIN 17 393 CALRETICULIN.  
 FT DOMAIN 189 254 4 X 12 AA APPROXIMATE REPEATS.  
 FT REPEAT 189 200 1-1.  
 FT REPEAT 209 220 1-2.  
 FT REPEAT 225 236 1-3.  
 FT REPEAT 243 254 1-4.  
 FT DOMAIN 257 295 3 X 11 AA APPROXIMATE REPEATS.  
 FT REPEAT 257 267 2-1.  
 FT REPEAT 271 281 2-2.  
 FT REPEAT 285 295 2-3.  
 FT CARBOHYD 27 27 N-LINKED (GLCNAC. .) (POTENTIAL).  
 FT DISULFID 135 161 BY SIMILARITY.  
 FT SITE 390 393 PREVENT SECRETION FROM ER.  
 FT CONFLICT 89 90 MV -> IL (IN REF. 2).  
 FT CONFLICT 188 207 MISSING (IN REF. 2).  
 FT CONFLICT 378 378 Y -> D (IN REF. 2).  
 SQ SEQUENCE 393 AA; 45397 MW; 45F59857C21940D2 CRC64;

Query Match 74.2%; Score 112; DB 1; Length 393;  
 Best Local Similarity 77.8%; Pred. No. 9.2e-09;  
 Matches 21; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

OY 1 CGPGTKKHVIFNYKGNVLINKDIRC 27  
 |||||  
 DB 135 CGMATKKHVIFNYKGNHLIKKEIPC 161

## RESULT 10

CRTC\_CHLRE  
 ID CRTC\_CHLRE STANDARD; PRT; 420 AA.  
 AC Q9STD3;  
 DT 20-AUG-2001 (Rel. 40, Created)  
 DT 20-AUG-2001 (Rel. 40, Last sequence update)  
 DT 20-AUG-2001 (Rel. 40, Last annotation update)  
 DE CALRETICULIN PRECURSOR.  
 OS Chlamydomonas reinhardtii.  
 OC Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;  
 OC Chlamydomonadaceae; Chlamydomonas.  
 OX NCBI\_TaxID=3055;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=137C;  
 RA Zuppin A., Kaydamov C.;  
 RT "Cloning and characterization of a cDNA encoding Chlamydomonas  
 RT reinhardtii calreticulin."  
 RL Submitted (Oct-1997) to the EMBL/GenBank/DBJ databases.  
 CC -!- FUNCTION: THIS PROTEIN BINDS CALCIUM. THERE ARE BOTH HIGH AND  
 CC LOW AFFINITY CALCIUM-BINDING SITES (BY SIMILARITY).

CC -1- SUBCELLULAR LOCATION: ENDOPLASMIC RETICULUM LUMEN (BY SIMILARITY).  
 CC -1- SIMILARITY: BELONGS TO THE CALRETICULIN FAMILY.  
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 CC -----  
 CC EMBL: AJ000765; CAB54526.1; -  
 CC InterPro: IPR001580; Calreticulin.  
 CC InterPro: IPR000886; ER-target.  
 CC Pfam: PF00262; calreticulin.1.  
 CC PRINTS: PR00626; CALRETICULIN.  
 CC PRODOM: PD001866; Calreticulin; 1.  
 CC PROSITE: PS00014; ER-TARGET; 1.  
 CC PROSITE: PS00803; CALRETICULIN\_1; 1.  
 CC PROSITE: PS00804; CALRETICULIN\_2; 1.  
 CC PROSITE: PS00805; CALRETICULIN\_REPEAT; 1.  
 CC Endoplasmic reticulum; Calcium-binding; Repeat; Signal.  
 CC SIGNAL 1 18 POTENTIAL.  
 CC CHAIN 19 420 CALRETICULIN.  
 CC SITE 417 420 PREVENT SECRETION FROM ER (POTENTIAL).  
 CC SEQUENCE 420 AA; 47327 MW; DD3BA3AFBF61C9B CRC64;  
 CC -----  
 CC Query Match 64.2%; Score 97; DB 1; Length 420;  
 CC Best Local Similarity 69.2%; Pred. No. 1.4e-06;  
 CC Matches 18; Conservative 2; Mismatches 6; Indels 0; Gaps 0;  
 CC -----  
 CC QY 1 CGPCTKKVHVIFNYKGNVLINKDIR 26  
 CC || | : || || | || || | || || |  
 CC Db 140 CGYSTRKVVHILYKGNVLIKKDIK 165  
 CC -----  
 CC RESULT 11  
 CC CRIC.CAEEL  
 CC ID CRIC.CAEEL STANDARD; PRT; 395 AA.  
 CC AC P27798;  
 CC DT 01-AUG-1992 (Rel. 23, Created)  
 CC DT 01-AUG-1992 (Rel. 23, Last sequence update)  
 CC DT 01-FEB-1994 (Rel. 28, Last annotation update)  
 CC DE CALRETICULIN PRECURSOR.  
 CC GIN CRT-1.  
 CC OX Caenorhabditis elegans.  
 CC OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;  
 CC Rhabditidae; Peloderinae; Caenorhabditis.  
 CC OX NCBI\_TaxID:6239;  
 CC [1]  
 CC RN SEQUENCE FROM N.A.  
 CC RC STRAIN-BRISTOL N2;  
 CC RX MEDLINE 92329978; PubMed 1627827;  
 CC Smith M.J.;  
 CC "A.C. elegans gene encodes a protein homologous to mammalian  
 CC calreticulin".  
 CC RT DNA Seq. 2:235-240(1992).  
 CC RL -1- FUNCTION: THIS PROTEIN BINDS CALCIUM. THERE ARE BOTH HIGH AND  
 CC LOW AFFINITY CALCIUM-BINDING SITES.  
 CC -1- SUBCELLULAR LOCATION: ENDOPLASMIC RETICULUM LUMEN.  
 CC -1- SIMILARITY: BELONGS TO THE CALRETICULIN FAMILY.  
 CC -----  
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 CC -----  
 CC EMBL: X59589; CAA42159.1; -  
 CC PIR: S25851; S25851.

DR InterPro: IPR001580; Calreticulin.  
 DR InterPro: IPR000886; ER-target.  
 DR Pfam: PF00262; calreticulin.1.  
 DR PRINTS: PR00626; CALRETICULIN.  
 DR PRODOM: PD001866; Calreticulin; 1.  
 DR PROSITE: PS00014; ER-TARGET; 1.  
 DR PROSITE: PS00803; CALRETICULIN\_1; 1.  
 DR PROSITE: PS00804; CALRETICULIN\_2; 1.  
 DR PROSITE: PS00805; CALRETICULIN\_REPEAT; 3.  
 DR Endoplasmic reticulum; Calcium-binding; Repeat; Signal.  
 DR KW SIGNAL 1 395 POTENTIAL.  
 DR FT CHAIN ? 395 CALRETICULIN.  
 DR FT DOMAIN ? 192 N-DOMAIN.  
 DR FT DOMAIN 193 301 P-DOMAIN.  
 DR FT DOMAIN 302 395 C-DOMAIN.  
 DR FT DOMAIN 186 250 4 X APPROXIMATE REPEATS.  
 DR FT REPEAT 186 197 1-1.  
 DR FT REPEAT 205 216 1-2.  
 DR FT REPEAT 222 233 1-3.  
 DR FT REPEAT 239 250 1-4.  
 DR FT DOMAIN 254 292 3 X APPROXIMATE REPEATS.  
 DR FT REPEAT 254 284 2-1.  
 DR FT REPEAT 268 278 2-2.  
 DR FT REPEAT 282 292 2-3.  
 DR FT DOMAIN 332 390 ASP/GLU/LYS-RICH.  
 DR FT DISULFID 133 158 BY SIMILARITY.  
 DR FT SITE 392 395 PREVENT SECRETION FROM ER.  
 DR SQ SEQUENCE 395 AA; 45616 MW; 35CA7D2EC1D56B03 CRC64;  
 CC -----  
 CC Query Match 63.9%; Score 96.5; DB 1; Length 395;  
 CC Best Local Similarity 66.7%; Pred. No. 1.5e-06;  
 CC Matches 18; Conservative 4; Mismatches 4; Indels 1; Gaps 1;  
 CC -----  
 CC QY 1 CGPCTKKVHVIFNYKGNVLINKDIR 27  
 CC || | : || || | || || | || || |  
 CC Db 133 CGP-TRRVHILYKGNVLIKKKEITC 158  
 CC -----  
 CC RESULT 12  
 CC CRIC.BETVU  
 CC ID CRIC.BETVU STANDARD; PRT; 416 AA.  
 CC AC O81919;  
 CC DT 20-AUG-2001 (Rel. 40, Created)  
 CC DT 20-AUG-2001 (Rel. 40, Last sequence update)  
 CC DT 20-AUG-2001 (Rel. 40, Last annotation update)  
 CC DE CALRETICULIN PRECURSOR.  
 CC OS Beta vulgaris (Sugar beet).  
 CC OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 CC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 CC Caryophyllidae; Caryophyllales; Chenopodiaceae; Beta.  
 CC OX NCBI\_TaxID:3555;  
 CC [1]  
 CC RN SEQUENCE FROM N.A.  
 CC RC STRAIN-VV-D/ZR5; TISSUE-Leaf;  
 CC RA Viereck R.;  
 CC RT "Nucleotide sequence from sugar beet calreticulin".  
 CC RL Submitted (OC-1997) to the EMBL/GenBank/DBJ databases.  
 CC -1- FUNCTION: THIS PROTEIN BINDS CALCIUM. THERE ARE BOTH HIGH AND  
 CC LOW AFFINITY CALCIUM-BINDING SITES (BY SIMILARITY).  
 CC -1- SUBCELLULAR LOCATION: ENDOPLASMIC RETICULUM LUMEN (BY SIMILARITY).  
 CC -1- SIMILARITY: BELONGS TO THE CALRETICULIN FAMILY.  
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 CC -----  
 CC EMBL: AJ002057; CAA05161.1; -  
 CC PIR: S2549; Betvu.1166; 32549.

DR InterPro; IPR001580; Calreticulin.

DR InterPro; IPR000886; ER\_target.

DR Pfam; PF00262; calreticulin; 1.

DR PRINTS; PR00626; CALRETICULIN.

DR ProDom; PD001866; Calreticulin; 1.

DR PROSITE; PS00014; ER\_TARGET; 1.

DR PROSITE; PS00803; CALRETICULIN\_1; 1.

DR PROSITE; PS00804; CALRETICULIN\_2; 1.

DR PROSITE; PS00805; CALRETICULIN\_REPEAT; 2.

KW Endoplasmic reticulum; Calcium-binding; Repeat; Signal; Glycoprotein.

FT SIGNAL 1 25 POTENTIAL.

FT CHAIN 26 46 CALRETICULIN.

FT CARBOHYD 57 57 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 157 157 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT SITE 413 416 PREVENT SECRETION FROM ER (POTENTIAL).

SQ SEQUENCE 416 AA: 48136 MW; 565FEC3489F77CA7 CRC64;

Query Match 60.9%; Score 92; DB 1; Length 416;

Best Local Similarity 63.0%; Pred. No. 7; le-06;

Matches 17; Conservative 1; Mismatches 9; Indels 0; Gaps 0;

QY 1 CGPGTKKHVIFNYKGNVLINKDIRC 27

DB 143 CGYSTKKVHAIFNYDNTNHLIKKDVPC 169

RESULT 13

CRTC\_ARATH

ID CRTC\_ARATH STANDARD; PRT: 424 AA.

AC 004153; Q9SJE7;

DT 20-AUG-2001 (Rel. 40, Created)

DT 20-AUG-2001 (Rel. 40, Last sequence update)

DT 20-AUG-2001 (Rel. 40, Last annotation update)

DE CALRETICULIN 3 PRECURSOR.

GN CRTC OR T27G7.13.

OS Arabidopsis thaliana (Mouse-ear cress).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;

OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.

OX NCBI\_TaxID=3702;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=97303616; PubMed=9159940;

RA Nelson D.E., Glaunsinger B., Bohnert H.J.;

RT "Abundant accumulation of the calcium-binding molecular chaperone

calreticulin in specific floral tissues of Arabidopsis thaliana.";

RL Plant Physiol. 114:29-37(1997).

RN [2]

RP SEQUENCE FROM N.A.

RA Shinn P., Brooks S., Buehler E., Chao Q., Johnson-Hopson C., Khan S.,

RA Kim C., Altafi H., Bei O., Chin C., Chiou J., Choi E., Conn L.,

RA Conway A., Gonzales A., Hansen N., Howing B., Koo T., Lam B., Lee J.,

RA Lenz C., Li J., Liu A., Liu K., Liu S., Mukharsky N., Nguyen M.,

RA Palm C., Pham P., Sakano H., Schwartz J., Southwick A., Thaveri A.,

RA Toriumi M., Vaysberg M., Yu G., Federspiel N.A., Theologis A.,

RA Ecker J.R.;

RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.

CC -!- FUNCTION: THIS PROTEIN BINDS CALCIUM. THERE ARE BOTH HIGH AND

LOW AFFINITY CALCIUM-BINDING SITES (BY SIMILARITY).

CC -!- SUBCELLULAR LOCATION: ENDOPLASMIC RETICULUM LUMEN (BY SIMILARITY).

CC -!- SIMILARITY: BELONGS TO THE CALRETICULIN FAMILY.

CC -----

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CC -----

DR EMBL; U66345; AAC49697.1; "

DR EMBL; AC006932; AAF22902.1; ALT\_SEQ.

DR Mendel; 16507; Arath;1166;16507.

DR InterPro; IPR001580; Calreticulin.

DR InterPro; IPR000886; ER\_target.

DR Pfam; PF00262; calreticulin; 1.

DR PRINTS; PR00626; CALRETICULIN.

DR ProDom; PD001866; Calreticulin; 1.

DR PROSITE; PS00014; ER\_TARGET; 1.

DR PROSITE; PS00803; CALRETICULIN\_1; 1.

DR PROSITE; PS00804; CALRETICULIN\_2; 1.

DR PROSITE; PS00805; CALRETICULIN\_REPEAT; 1.

KW Endoplasmic reticulum; Calcium-binding; Repeat; Signal; Glycoprotein;

KW Multigene family.

FT SIGNAL 1 28 POTENTIAL.

FT CHAIN 29 424 CALRETICULIN 3.

FT CARBOHYD 97 97 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT SITE 421 424 PREVENT SECRETION FROM ER (POTENTIAL).

FT CONFLICT 279 279 F -> S (IN REF. 2).

SQ SEQUENCE 424 AA: 49904 MW; 650E0AE8342F0B97 CRC64;

Query Match 58.3%; Score 88; DB 1; Length 424;

Best Local Similarity 55.6%; Pred. No. 2; 7e-05;

Matches 15; Conservative 6; Mismatches 6; Indels 0; Gaps 0;

QY 1 CGPGTKKHVIFNYKGNVLINKDIRC 27

DB 146 CGQTQTKLHVIVSYQGQNPYIKKDLQC 172

RESULT 14

CRTC\_PUJAR

ID CRTC\_PUJAR STANDARD; PRT: 421 AA.

AC Q9XF98;

DT 20-AUG-2001 (Rel. 40, Created)

DT 20-AUG-2001 (Rel. 40, Last sequence update)

DT 20-AUG-2001 (Rel. 40, Last annotation update)

DE CALRETICULIN PRECURSOR.

OS Prunus armeniaca (Apricot).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;

OC eurosids I; Rosales; Rosaceae; Prunus.

OX NCBI\_TaxID=36596;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=CV. BERGERON; TISSUE=Mesocarp, and Endocarp;

RA Mbeguie-A-Mbeguie D., Fills-Lycaon B.R.;

RT "Molecular cloning and nucleotide sequence of a calreticulin from

apricot (Prunus armeniaca cv. Bergeron).";

RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.

CC -!- FUNCTION: THIS PROTEIN BINDS CALCIUM. THERE ARE BOTH HIGH AND

LOW AFFINITY CALCIUM-BINDING SITES (BY SIMILARITY).

CC -!- SUBCELLULAR LOCATION: ENDOPLASMIC RETICULUM LUMEN (BY SIMILARITY).

CC -!- SIMILARITY: BELONGS TO THE CALRETICULIN FAMILY.

CC -----

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CC -----

DR EMBL; AFL34733; AAD32207.1; "

DR InterPro; IPR001580; Calreticulin.

DR InterPro; IPR000886; ER\_target.

DR Pfam; PF00262; calreticulin; 1.

DR PRINTS; PR00626; CALRETICULIN.

DR ProDom; PD001866; Calreticulin; 1.

DR PROSITE; PS00014; ER\_TARGET; 1.

DR PROSITE; PS00803; CALRETICULIN\_1; 1.

DR PROSITE; PS00804; CALRETICULIN\_2; 1.

DR PROSITE; PS00805; CALRETICULIN\_REPEAT; 2.

KW Endoplasmic reticulum; Calcium-binding; Repeat; Signal; Glycoprotein.



GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: January 9, 2002, 15:02:02 ; Search time 43.73 Seconds  
(without alignments)  
47.032 Million cell updates/sec

Title: US-09-828-000-5  
Perfect score: 151  
Sequence: 1 CGPGTKKHVIFNYKGNVLINKDIRC 27  
Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues  
Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR\_68.\*  
1: pir1.\*  
2: pir2.\*  
3: pir3.\*  
4: pir4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	151	100.0	400	2 S43376	calreticulin, brai
2	151	100.0	416	1 S06763	calreticulin precu
3	151	100.0	416	2 JH0819	calreticulin precu
4	151	100.0	417	1 A37047	calreticulin precu
5	151	100.0	418	1 A34154	calreticulin precu
6	151	100.0	421	2 S36799	calreticulin precu
7	141	93.4	405	1 JH0795	calreticulin precu
8	134	88.7	406	2 A56637	calreticulin homol
9	125	82.8	419	2 S71343	calreticulin precu
10	121	80.1	336	2 A32507	41K larval antigen
11	120	79.5	384	2 S29130	calreticulin (clon
12	120	79.5	411	2 S29129	calreticulin precu
13	112	74.2	393	1 A48573	calreticulin autoa
14	96.5	63.9	395	2 S25851	calreticulin precu
15	92	60.9	416	2 T14554	calreticulin - bee
16	84	55.6	412	2 T05703	calreticulin - bar
17	84	55.6	415	2 T05705	calreticulin - bar
18	83	55.0	421	2 S58170	calreticulin precu
19	83	55.0	425	2 C96605	calreticulin (Ctrl
20	82	54.3	415	2 T10172	calreticulin - cas
21	80	53.0	422	2 T07841	probable calreticu
22	79	52.3	444	2 H86224	hypothetical prote
23	76	50.3	389	2 T03691	calreticulin - com
24	76	50.3	416	2 T16968	calreticulin call
25	54	35.8	720	2 T43854	helicase [imported
26	53	35.1	464	2 A53101	vitamin D3 hydroxy
27	53	35.1	764	2 F83161	pyocin protein PA3
28	52	34.4	1938	1 MNKWL	myosin heavy chain
29	51	33.8	560	2 S50439	hypothetical prote

ALIGNMENTS

```
RESULT 1
S43376
calreticulin, brain isoform 1 - bovine
C:Species: Bos primigenius taurus (cattle)
C>Date: 20-Oct-1994 #sequence_revision 23-Mar-1995 #text_change 07-May-1999
C:Accession: S43376; S36801
R:Matsuoka, K.; Seta, K.; Yamakawa, Y.; Okuyama, T.; Shinoda, T.; Isobe, T.
Biochem. J. 298, 435-442, 1994
A:Title: Covalent structure of bovine brain calreticulin.
A:Reference number: S43376; MUID:94183174
A:Accession: S43376
A:Molecule type: protein
A:Residues: 1-400 <MAT>
A:Experimental source: brain
R:Liu, N.; Fine, R.E.; Johnson, R.J.
Biochim. Biophys. Acta 1202, 70-76, 1993
A:Title: Comparison of cDNAs from bovine brain coding for two isoforms of calreticuli
A:Reference number: S36799; MUID:93385184
A:Accession: S36801
A>Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 45-63, 'E', 65-83 <LIU>
A:Experimental source: brain, clone 8.1
C:Superfamily: calreticulin
C:Keywords: calcium binding; glycoprotein
F:397-400/Region: endoplasmic reticulum retention signal
F:120-146/Disulfide bonds: #status experimental
F:162/Binding site: carbohydrate (Asn) (covalent) #status experimental

Query Match 100.0%; Score 151; DB 2; Length 400;
Best Local Similarity 100.0%; Pred. No. 3.5e-14;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGPGTKKHVIFNYKGNVLINKDIRC 27
Db 120 CGPGTKKHVIFNYKGNVLINKDIRC 146

RESULT 2
S06763
calreticulin precursor - mouse
N:Alternate names: 55K calcium-binding reticuloplasmin; calregulin
C:Species: Mus musculus (house mouse)
C>Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C:Accession: S06763; JCI1444; PCI1233; A57498
R:Smith, M.J.; Koch, G.L.E.
EMBO J. 8, 3581-3586, 1989
A:Title: Multiple zones in the sequence of calreticulin (CRP55, calregulin, HACBP), a
A:Reference number: S06763; MUID:90059955
A:Accession: S06763
A:Molecule type: DNA
```

A:Residues: 1-416 <SMI>  
A:Cross-references: EMBL:X14926; NID:g50567; PIDN:CAA33053.1; PID:g50568  
R:Marzarella, B.A.; Gold, P.; Cunningham, M.; Green, M.  
Gene 120, 217-225, 1992  
A:Title: Determination of the sequence of an expressible cDNA clone encoding Erp60/calreticulin  
A:Reference number: JCI1444; MUID:93013037  
A:Accession: JCI1444  
A:Molecule type: mRNA  
A:Residues: 1-416 <MAZ>  
A:Cross-references: GB:M92988; NID:g193084; PIDN:AAA37569.1; PID:g193085  
A:Accession: PC1233  
A:Molecule type: protein  
A:Residues: 18-41 <MAZ>  
R:White, T.K.; Zhu, Q.; Tanzer, M.L.  
J. Biol. Chem. 270, 15926-15929, 1995  
A:Title: Cell surface calreticulin is a putative mannoside lectin which triggers mouse m  
A:Reference number: A57498; MUID:95332280  
A:Accession: A57498  
A:Status: preliminary  
A:Molecule type: protein  
A:Residues: 74-80:142-151:186-193 <WHI>  
C:Superfamily: calreticulin  
C:Keywords: calcium binding  
F:1-17/Domain: signal sequence #status predicted <SIG>  
F:18-416/Product: calregulin #status experimental <MAT>  
F:413-416/Region: endoplasmic reticulum retention signal

Query Match 100.0%; Score 151; DB 1; Length 416;  
Best Local Similarity 100.0%; Pred. No. 3.6e-14;  
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGPGTKKVVHVIENYKGNVINKDIRC 27  
|||||  
DB 137 CGPGTKKVVHVIENYKGNVINKDIRC 163

RESULT 3  
JH0819  
calreticulin precursor - rat  
N:Alternate names: calcium-binding protein 3  
C:Species: Rattus norvegicus (Norway rat)  
C:Date: 30-Sep-1993 #sequence\_revision 20-Aug-1994 #text\_change 20-Jun-2000  
C:Accession: JH0819; A49176; S11205; PC1109; S45036; S04867; S39372; A34473; S13045  
R:Nakamura, M.; Moriye, M.; Baba, T.; Michikawa, Y.; Yamanobe, T.; Arai, K.; Okinaga, S.  
Exp. Cell Res. 205, 101-110, 1993  
A:Title: An endoplasmic reticulum protein, calreticulin, is transported into the acrosom  
A:Reference number: A49176; MUID:93202172  
A:Accession: JH0819  
A:Molecule type: mRNA  
A:Residues: 1-416 <NAK>  
A:Cross-references: GB:D78308; NID:g1089798; PIDN:BA11345.1; PID:g1845572  
A:Accession: A49176  
A:Status: preliminary  
A:Molecule type: protein  
A:Residues: 1-416 <NAZ>  
A:Cross-references: GB:D78308; NID:g1089798; PIDN:BA11345.1; PID:g1845572  
A:Experimental source: Sprague-Dawley, spermatogenic cells  
A:Note: sequence extracted from NCHI backbone (NCBI:127639, NCBI:127643)  
R:Murthy, K.K.; Banville, D.; Strikant, C.B.; Carrier, F.; Holmes, C.; Bell, A.; Patel, Y.  
Nucleic Acids Res. 18, 4933, 1990  
A:Title: Structural homology between the rat calreticulin gene product and the Onchocerc  
A:Reference number: S11205; MUID:90370496  
A:Accession: S11205  
A:Molecule type: mRNA  
A:Residues: 1-416 <MUR>  
A:Cross-references: EMBL:X53363; NID:g55854; PIDN:CAA37446.1; PID:g55855  
R:Nakamura, M.; Michikawa, Y.; Baba, T.; Okinaga, S.; Arai, K.  
Biochem. Biophys. Res. Commun. 186, 668-673, 1992  
A:Title: Calreticulin is present in the acrosome of spermatids of rat testis.  
A:Reference number: PC1109; MUID:92360010  
A:Accession: PC1109  
A:Molecule type: protein

A:Residues: 18-32 <NAK2>  
A:Experimental source: testis, strain Sprague-Dawley  
R:Soennichsen, B.; Fuellekrug, J.; van Nguyen, P.; Diekmann, W.; Robinson, D.G.; Mies  
submitted to the EMBL Data Library, May 1994  
A:Description: Retention and retrieval: both mechanisms cooperate to maintain calret  
A:Reference number: S45036  
A:Accession: S45036  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-416 <SO>  
A:Cross-references: EMBL:X79327; NID:g488840; PIDN:CAA55890.1; PID:g488841  
R:Lone, Y.C.; Bailly, A.; Latruffe, N.  
submitted to the EMBL Data Library, December 1988  
A:Reference number: S04867  
A:Accession: S04867  
A:Molecule type: mRNA  
A:Residues: 'R', 270-358, 'AAG' <LON>  
A:Cross-references: EMBL:X13702; NID:g56055; PIDN:CAA31987.1; PID:g930260  
A:Note: the authors designated the protein as D-beta-hydroxybutyrate dehydrogenase  
R:Yokoi, T.; Nagayama, S.; Kajiwara, R.; Kawaguchi, Y.; Horiuchi, R.; Kamataki, T.  
Biochim. Biophys. Acta 1158, 339-344, 1993  
A:Title: Identification of protein disulfide isomerase and calreticulin as autoimmune  
A:Reference number: S39371; MUID:94072621  
A:Accession: S39372  
A:Molecule type: protein  
A:Residues: 18-23, 'X', 25-32 <YOK>  
R:Van, P.N.; Peter, F.; Soelling, H.D.  
J. Biol. Chem. 264, 17494-17501, 1989  
A:Title: Four intracisternal calcium-binding glycoproteins from rat liver microsomes  
itive calcium sequestering rat liver vesicles.  
A:Reference number: A34473; MUID:90008920  
A:Accession: A34473  
A:Status: preliminary  
A:Molecule type: protein  
A:Residues: 18-36 <VAN>  
R:Troves, S.; de Mattei, M.; Lanfredi, M.; Villa, A.; Green, N.M.; MacLennan, D.H.; M  
Biochem. J. 271, 473-480, 1990  
A:Title: Calreticulin is a candidate for a calsequestrin-like function in Ca(2+)-stor  
A:Reference number: S13045; MUID:91054414  
A:Accession: S13045  
A:Molecule type: protein  
A:Residues: 18-29 <TRE>  
C:Superfamily: calreticulin  
C:Keywords: calcium binding; glycoprotein  
F:1-17/Domain: signal sequence #status predicted <SIG>  
F:18-416/Product: calreticulin #status experimental <MAT>  
F:204-212/Region: nuclear location signal  
F:413-416/Region: endoplasmic reticulum retention signal  
F:344/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 100.0%; Score 151; DB 2; Length 416;  
Best Local Similarity 100.0%; Pred. No. 3.6e-14;  
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGPGTKKVVHVIENYKGNVINKDIRC 27  
|||||  
DB 137 CGPGTKKVVHVIENYKGNVINKDIRC 163

RESULT 4  
A37047  
calreticulin precursor - human  
N:Alternate names: 52K ribonucleoprotein autoantigen Ro/SS-A; 60K integrin-binding pr  
C:Species: Homo sapiens (man)  
C:Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 18-Feb-2000  
C:Accession: A42330; A37047; A46452; A28812; PH1525; A40346; S11475; T45075  
R:McCaulliffe, D.P.; Yang, Y.S.; Wilson, J.; Sontheimer, R.D.; Capra, J.D.  
J. Biol. Chem. 267, 2557-2562, 1992  
A:Title: The 5'-flanking region of the human calreticulin gene shares homology with t  
A:Reference number: A42330; MUID:92129342  
A:Accession: A42330  
A:Molecule type: DNA

A:Residues: 1-417 <MC2>  
A:Note: sequence extracted from NCBI backbone (NCBIN:78537, NCBIP:78536)  
R:McCaulliffe, D.P.; Lux, F.A.; Lieu, T.S.; Sanz, I.; Hanke, J.; Newkirk, M.M.; Bachinski  
J. Clin. Invest. 85, 1379-1391, 1990  
A:Title: Molecular cloning, expression, and chromosome 19 localization of a human Ro/SS-  
A:Reference number: A37047; MUID:90237213  
A:Accession: A37047  
A:Molecule type: mRNA  
A:Residues: 1-417 <MC2>  
A:CROSS-references: GB:M32294; NID:g337486; PIDN:AAA36582.1; PID:g337487  
A:Note: the authors translated the codon CTA for residue 349 as Tyr  
R:Roelach, L.A.; Haselby J.A.; Mellof, J.F.; Smeenk, R.J.; Unnasch, T.R.; Greene, B.M.;  
J. Immunol. 147, 3031-3039, 1991  
A:Title: Characterization of the autoantigen calreticulin.  
A:Reference number: A46452; MUID:92013129  
A:Accession: A46452  
A:Molecule type: mRNA  
A:Residues: 1-417 <ROK>  
A:CROSS-references: GB:M84739; NID:gl79881; PIDN:AAA51916.1; PID:gl79882  
A:Note: sequence extracted from NCBI backbone (NCBIN:60749, NCBIP:60750)  
R:Lieu, T.S.; Newkirk, M.M.; Capra, J.D.; Sontheimer, R.D.  
J. Clin. Invest. 82, 96-101, 1988  
A:Title: Molecular characterization of human Ro/SS-A antigen. Amino terminal sequence of  
A:Reference number: A28812; MUID:88273610  
A:Accession: A28812  
A:Molecule type: protein  
A:Residues: 18-41 <LIE>  
A:Note: 18-Ala was also found  
R:Dupuis, M.; Schaefer, E.; Krause, K.H.; Tschopp, J.  
J. Exp. Med. 177, 1-7, 1993  
A:Title: The calcium-binding protein calreticulin is a major constituent of lytic granul  
A:Reference number: PH1525; MUID:93115648  
A:Accession: PH1525  
A:Molecule type: protein  
A:Residues: 18-27 <DUP>  
A:Experimental source: LAK cell  
R:Roilani, M.V.; Finlay, B.B.; Gray, V.; Dedhar, S.  
Biochemistry 30, 9859-9866, 1991  
A:Title: In vitro interaction of a polypeptide homologous to human Ro/SS-A antigen (calr  
A:Reference number: A40346; MUID:92002034  
A:Accession: A40346  
A:Molecule type: protein  
A:Residues: 18-34, 'R' <ROU>  
R:Krause, K.H.; Simmerman, H.K.B.; Jones, L.R.; Campbell, K.P.  
Biochem. J. 270, 545-548, 1990  
A:Title: Sequence similarity of calreticulin with a Ca(2+)-binding protein that co-purif  
A:Reference number: S11475; MUID:90380058  
A:Accession: S11475  
A:Molecule type: protein  
A:Residues: 18-32 <KRA>  
R:Lamerdin, J.; McCready, P.; Stilwagen, S.; Ramirez, M.; Carrano, A.  
submitted to the EMBL Data Library, November 1996  
A:Description: Characterization by genomic sequence analysis of a gene-rich 111 kb regio  
A:Reference number: Z22906  
A:Accession: T45075  
A>Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-417 <LAW>  
A:CROSS-references: EMBL:AD000092; PIDN:AA851176.1  
A:Experimental source: cell line 5HL2-B; fibroblast  
C:Comment: Autoantibodies specific for this protein are found in Sjogren's syndrome and  
C:Genetics:  
A:Gene: GDB:CALR  
A:CROSS-references: GDB:125179; OMIM:109091  
A:Map position: 19p13.3-19p13.2  
A:Introns: 31/1; 65/1; 133/1; 164/3; 234/3; 272/3; 320/3; 351/3  
A:Note: CRTG  
C:Superfamily: calreticulin  
C:Keywords: calcium binding; integrin binding  
F:1-17/Domain: signal sequence #status predicted <SIG>  
F:18-417/Product: calreticulin #status predicted <MAT>  
F:141-167/Region: endoplasmic reticulum retention signal  
F:414-417/Region: endoplasmic reticulum retention signal

Query Match 100.0%; Score 151; DB 1; Length 417;  
Best Local Similarity 100.0%; Pred. No. 3.6e-14;  
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGPGTKKHVHFIENYKGNVLINKDIRC 27  
|||||  
DB 137 CGPGTKKHVHFIENYKGNVLINKDIRC 163

## RESULT 5

A34154  
calreticulin precursor, skeletal muscle - rabbit  
C:Species: Oryctolagus cuniculus (domestic rabbit)  
C:Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 10-Sep-1999  
R:Accession: A34154; S13047  
R:Fliegel, L.; Burns, K.; MacLennan, D.H.; Reithmeier, R.A.F.; Michalak, M.  
J. Biol. Chem. 264, 21522-21528, 1989  
A:Title: Molecular cloning of the high affinity calcium-binding protein (calreticulin  
A:Reference number: A34154; MUID:90094320  
A:Accession: A34154  
A>Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-418 <FLI>  
A:CROSS-references: GB:J05138; NID:gl64858; PIDN:AAA31188.1; PID:gl64859  
R:Treves, S.; de Mattei, M.; Lanfredi, M.; Villa, A.; Green, N.M.; MacLennan, D.H.; M  
Biochem. J. 271, 473-480, 1990  
A:Title: Calreticulin is a candidate for a calsequestrin-like function in Ca(2+)-stor  
A:Reference number: S13045; MUID:91054414  
A:Accession: S13047  
A:Molecule type: protein  
A:Residues: 19-32 <TRE>  
C:Superfamily: calreticulin  
C:Keywords: skeletal muscle  
F:1-17/Domain: signal sequence #status predicted <SIG>  
F:415-418/Region: endoplasmic reticulum retention signal

Query Match 100.0%; Score 151; DB 1; Length 418;  
Best Local Similarity 100.0%; Pred. No. 3.6e-14;  
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGPGTKKHVHFIENYKGNVLINKDIRC 27  
|||||  
DB 137 CGPGTKKHVHFIENYKGNVLINKDIRC 163

## RESULT 6

S36799  
calreticulin precursor, brain isoform 2 - bovine  
C:Species: Bos primigenius taurus (cattle)  
C:Date: 10-Dec-1993 #sequence\_revision 23-Mar-1995 #text\_change 13-Aug-1999  
R:Accession: S36799; S36800  
R:Liu, N.; Fine, R.E.; Johnson, R.J.  
Biochim. Biophys. Acta 1202, 70-76, 1993  
A:Title: Comparison of cDNAs from bovine brain coding for two isoforms of calreticuli  
A:Reference number: S36799; MUID:93385184  
A:Accession: S36799  
A:Molecule type: mRNA  
A:Residues: 1-421 <LIU>  
A:CROSS-references: GB:LI3462; NID:g348693; PIDN:AAC37307.1; PID:g348694  
A:Experimental source: brain, clone 9.4  
A:Accession: S36800  
A:Molecule type: protein  
A:Residues: 35-45 <LI2>  
C:Superfamily: calreticulin  
C:Keywords: calcium binding; glycoprotein  
F:1-34/Domain: signal sequence #status predicted <SIG>  
F:35-421/Product: calreticulin, brain isoform 2 #status predicted <MAT>  
F:418-421/Region: endoplasmic reticulum retention signal  
F:141-167/Disulfide bonds: #status predicted  
F:183/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 100.0%; Score 151; DB 2; Length 421;  
 Best Local Similarity 100.0%; Pred. No. 3,7e-14; Indels 0; Gaps 0;  
 Matches 27; Conservative 0; Mismatches 0; Gaps 0;

QY 1 CGPCTKKVHVIFNYKGNVLINKDIRC 27  
 |||||  
 DB 141 CGPCTKKVHVIFNYKGNVLINKDIRC 167

RESULT 7  
 JH0795  
 calreticulin precursor - California sea hare  
 N/Alternate names: protein 407  
 C/Species: Aplysia californica (California sea hare)  
 C/Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 10-Sep-1999  
 C/Accession: JH0795; B31409; F60977  
 R/Kennedy, T.E.; Kuhl, D.; Barzilai, A.; Sweatt, J.D.; Kandel, E.R.  
 Neuron 9, 1013-1024, 1992  
 A/Title: Long-term sensitization training in aplysia leads to an increase in calreticulin  
 A/Reference number: JH0795; MUID:93098937  
 A/Accession: JH0795  
 A/Molecule type: mRNA  
 A/Residues: 1-405 <KEN>  
 A/Cross-references: GB:S51239; NID:q262053; PIDN:AA824569.1; PID:q262054  
 A/Experimental source: abdominal ganglion and antral nervous system  
 R/Kennedy, T.E.; Gawinowicz, M.A.; Barzilai, A.; Kandel, E.R.; Sweatt, J.D.  
 Proc. Natl. Acad. Sci. U.S.A. 85, 7008-7012, 1988  
 A/Title: Sequencing of proteins from two-dimensional gels by using in situ digestion and  
 titon in Aplysia.  
 A/Reference number: A94207; MUID:88320566  
 A/Accession: B31409  
 A/Molecule type: protein  
 A/Residues: 'X', 17-28, 'X', 30-31 <KE>  
 R/Sweatt, J.D.; Kennedy, T.E.; Wager-Smith, K.; Gawinowicz, M.A.; Barzilai, A.; Karl, K.  
 Electrophoresis 10, 152-157, 1989  
 A/Title: Development of a database of amino acid sequences for proteins identified and  
 A/Reference number: A60977; MUID:89276264  
 A/Accession: F60977  
 A/Molecule type: protein  
 A/Residues: 'X', 17-28, 'X', 30-31 <SWP>  
 C/Superfamily: calreticulin  
 C/Keywords: calcium binding; endoplasmic reticulum  
 F/1-15/Domain: signal sequence #status predicted <SIG>  
 F/16-405/Product: calreticulin #status experimental <MAT>  
 F/402-405/Region: endoplasmic reticulum retention signal

Query Match 93.4%; Score 141; DB 1; Length 405;  
 Best Local Similarity 88.9%; Pred. No. 9.9e-13; Indels 0; Gaps 0;  
 Matches 24; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 CGPCTKKVHVIFNYKGNVLINKDIRC 27  
 |||||  
 DB 133 CGPCTKKVHVIFNYKGNVLINKDIRC 159

RESULT 8  
 A36637  
 calreticulin homolog precursor - fruit fly (Drosophila melanogaster)  
 N/Alternate names: RO/SS-A autoantigen/calreticulin homolog  
 C/Species: Drosophila melanogaster  
 C/Date: 11-Aug-1995 #sequence\_revision 11-Aug-1995 #text\_change 13-Aug-1999  
 C/Accession: A56637; A37158  
 R/Smith, M.J.  
 DNA Seq. 3, 247-250, 1992  
 A/Title: Nucleotide sequence of a Drosophila melanogaster gene encoding a calreticulin h  
 A/Reference number: A56637; MUID:93208374  
 A/Accession: A56637  
 A/Status: Preliminary  
 A/Molecule type: DNA  
 A/Residues: 1-406 <SMI>  
 A/Cross-references: GB:X64461; NID:g7685; PIDN:CAA45791.1; PID:g7686

A/Note: sequence extracted from NCBI backbone (NCBIN:128274, NCBI:128275)  
 R/McCaulliffe, D.P.; Zappi, E.; Lileu, T.S.; Michalak, M.; Sontheimer, R.D.; Capra, J.D  
 J. Clin. Invest. 86, 332-335, 1990  
 A/Title: A human RO/SS-A autoantigen is the homologue of calreticulin and is highly h  
 A/Reference number: A37158; MUID:90307981  
 A/Accession: A37158  
 A/Status: preliminary; nucleic acid sequence not shown; not compared with conceptual  
 A/Molecule type: DNA  
 A/Residues: 91-105, 'A', 107, 109-124; 182-183, 'L', 185-220 <MCC>  
 C/Genetics:  
 A/Gene: FlyBase:Crc  
 A/Cross-references: FlyBase:FBgn0005585  
 A/Introns: 65/1; 222/3  
 C/Superfamily: calreticulin  
 C/Keywords: calcium binding; endoplasmic reticulum  
 F/1-17/Domain: signal sequence #status predicted <SIG>  
 F/403-406/Region: endoplasmic reticulum retention signal

Query Match 88.7%; Score 134; DB 2; Length 406;  
 Best Local Similarity 88.9%; Pred. No. 1e-11; Indels 0; Gaps 0;  
 Matches 24; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 CGPCTKKVHVIFNYKGNVLINKDIRC 27  
 |||||  
 DB 137 CGPCTKKVHVIFNYKGNVLINKDIRC 163

RESULT 9  
 S71343  
 calreticulin precursor - Korean frog  
 C/Species: Rana rugosa (Korean frog)  
 C/Date: 29-Jan-1998 #sequence\_revision 13-Feb-1998 #text\_change 20-Jun-2000  
 C/Accession: S71343  
 R/Yamamoto, S.; Nakamura, M.  
 FEBS Lett. 387, 27-32, 1996  
 A/Title: Calnexin: its molecular cloning and expression in the liver of the frog, Ran  
 A/Reference number: S71342; MUID:96234004  
 A/Accession: S71343  
 A/Status: nucleic acid sequence not shown  
 A/Molecule type: mRNA  
 A/Residues: 1-419 <YAM>  
 A/Cross-references: EMBL:D78589; NID:g1514956; PIDN:BAAL1425.1; PID:g1514957  
 C/Superfamily: calreticulin  
 C/Keywords: calcium binding; endoplasmic reticulum  
 F/1-18/Domain: signal sequence #status predicted <SIG>  
 F/19-419/Product: calreticulin #status predicted <MAT>  
 F/205-213/Region: nuclear location signal  
 F/415-418/Region: endoplasmic reticulum retention signal

Query Match 82.8%; Score 125; DB 2; Length 419;  
 Best Local Similarity 88.5%; Pred. No. 2.1e-10; Indels 0; Gaps 0;  
 Matches 23; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 CGPCTKKVHVIFNYKGNVLINKDIR 26  
 |||||  
 DB 138 CGPCTKKVHVIFNYKGNVLINKDIR 163

RESULT 10  
 A32507  
 41k larval antigen - nematode (Onchocerca volvulus) (fragment)  
 C/Species: Onchocerca volvulus  
 C/Date: 21-May-1990 #sequence\_revision 21-May-1990 #text\_change 12-Apr-1995  
 C/Accession: A32507; A28813  
 R/Unnasch, T.R.; Gallin, M.V.; Soboslay, P.T.; Erttmann, K.D.; Greene, B.M.  
 J. Clin. Invest. 82, 262-269, 1988  
 A/Title: Isolation and characterization of expression cDNA clones encoding antigens o  
 A/Reference number: A92769; MUID:88273584  
 A/Accession: A32507  
 A/Molecule type: mRNA  
 A/Residues: 1-336 <UNN>



C:Superfamily: calreticulin

Query Match 80.1%; Score 121; DB 2; Length 336;  
Best Local Similarity 77.8%; Pred. No. 6.5e-10;  
Matches 21; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 CGPGTKKHVIFNYKGNVLINKDIRC 27  
|||||  
Db 83 CGPGTKKHVIFNYKGNVLINKDIRC 109

## RESULT 11

S29130  
calreticulin (clone 8) - African clawed frog (fragment)  
C:Species: Xenopus laevis (African clawed frog)  
C:Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 13-Aug-1999  
C:Accession: S29130; T01068  
R:Treves, S.; Zorzato, F.; Pozzan, T.  
Biochem. J. 287, 579-581, 1992  
A:Title: Identification of calreticulin isoforms in the central nervous system.  
A:Reference number: S29129; MUID:93074997  
C:Accession: S29130  
A:Molecule type: mRNA  
A:Residues: 1-384 <TRE>  
A:Cross-references: EMBL:X67598  
A:Accession: T01068  
A:Status: translated from GB/EMBL/DBDJ  
A:Molecule type: mRNA  
A:Residues: 1-339, 'XTGR' <TRW>  
A:Cross-references: EMBL:X67598; NID:964610; PIDN:CAA47867.1; PID:964611  
A:Experimental source: CNS  
C:Superfamily: calreticulin  
C:Keywords: glycoprotein  
F:381-384/Region: endoplasmic reticulum retention signal  
F:316/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 79.5%; Score 120; DB 2; Length 384;  
Best Local Similarity 81.5%; Pred. No. 1e-09;  
Matches 22; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 CGPGTKKHVIFNYKGNVLINKDIRC 27  
|||||  
Db 109 CGPPTKKVHVIFQYKKNLQINKDIRC 135

## RESULT 12

S29129  
calreticulin precursor (clone 3) - African clawed frog (fragment)  
C:Species: Xenopus laevis (African clawed frog)  
C:Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 13-Aug-1999  
C:Accession: S29129  
R:Treves, S.; Zorzato, F.; Pozzan, T.  
Biochem. J. 287, 579-581, 1992  
A:Title: Identification of calreticulin isoforms in the central nervous system.  
A:Reference number: S29129; MUID:93074997  
C:Accession: S29129  
A:Molecule type: mRNA  
A:Residues: 1-411 <TRE>  
A:Cross-references: EMBL:X67597; NID:964608; PIDN:CAA47866.1; PID:964609  
C:Superfamily: calreticulin  
C:Keywords: glycoprotein  
F:1-12/Domain: signal sequence (fragment) #status predicted <SIG>  
F:13-411/Product: calreticulin #status predicted <MAT>  
F:408-411/Region: endoplasmic reticulum retention signal  
F:339/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 79.5%; Score 120; DB 2; Length 411;  
Best Local Similarity 81.5%; Pred. No. 1.1e-09;  
Matches 22; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 CGPGTKKHVIFNYKGNVLINKDIRC 27  
|||||  
Db 132 CGPPTKKVHVIFQYKKNLQINKDIRC 158

## RESULT 13

A48573  
calreticulin autoantigen homolog precursor - fluke (Schistosoma mansoni)  
C:Species: Schistosoma mansoni  
C:Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 10-Sep-1999  
C:Accession: A48573  
R:Khalife, J.; Trottein, F.; Schacht, A.M.; Godin, C.; Pierce, R.J.; Capron, A.  
Mol. Biochem. Parasitol. 57, 193-202, 1993  
A:Title: Cloning of the gene encoding a Schistosoma mansoni antigen homologous to hum  
A:Reference number: A48573; MUID:93165070  
C:Accession: A48573  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-393 <KHA>  
A:Cross-references: GB:M93097; NID:gl60928  
A:Note: sequence inconsistent with the nucleotide translation  
A:Note: sequence extracted from NCBI backbone (NCBIN:125085, NCBIP:125086)  
C:Superfamily: calreticulin  
F:1-16/Domain: signal sequence  
F:390-393/Region: endoplasmic reticulum retention signal

Query Match 74.2%; Score 112; DB 1; Length 393;  
Best Local Similarity 77.8%; Pred. No. 1.5e-08;  
Matches 21; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 1 CGPGTKKHVIFNYKGNVLINKDIRC 27  
|||||  
Db 135 CGMATKKVHVIFNYKGNHLIKKEIPC 161

## RESULT 14

S25851  
calreticulin precursor - Caenorhabditis elegans  
C:Species: Caenorhabditis elegans  
C:Date: 06-Jan-1994 #sequence\_revision 10-Nov-1995 #text\_change 05-Nov-1999  
C:Accession: S25851; T33996  
R:Smith, M.J.  
DNA Seq. 2, 235-240, 1992  
A:Title: A C. elegans gene encodes a protein homologous to mammalian calreticulin.  
A:Reference number: S25851; MUID:92329978  
C:Accession: S25851  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-395 <SMI>  
A:Cross-references: EMBL:X59589; NID:g6693; PIDN:CAA42159.1; PID:g6694  
R:Bauer, C.; Courtney, L.; Laplant, Y.  
submitted to the EMBL Data Library, February 1999  
A:Description: The sequence of C. elegans cosmid Y38A10A.  
A:Reference number: Z21453  
C:Accession: T33996  
A:Status: preliminary; translated from GB/EMBL/DBDJ  
A:Molecule type: DNA  
A:Residues: 1-395 <BAU>  
A:Cross-references: EMBL:AF125963; PIDN:AAD14746.1; GSPDB:GN00023; CESP:Y38A10A.5  
A:Experimental source: strain Bristol N2; clone Y38A10A  
C:Genetics:  
A:Gene: CESP:Y38A10A.5  
A:Map position: 5  
A:Introns: 107/3; 315/3  
C:Superfamily: calreticulin  
F:1-15/Domain: signal sequence #status predicted <SIG>  
F:392-395/Region: endoplasmic reticulum retention signal

Query Match 63.9%; Score 96.5; DB 2; Length 395;  
Best Local Similarity 66.7%; Pred. No. 2.7e-06;  
Matches 18; Conservative 4; Mismatches 4; Indels 1; Gaps 1;

QY 1 CGPCTKKVHVNIYKGNVLIINKDIRC 27  
Db 133 CGP-TRRVHVLINYNKGNLIINKKEITC 158  
RESULT 15  
T14554  
calreticulin - beet  
C:Species: Beta vulgaris (beet)  
C:Date: 20-Sep-1999 #sequence\_revision 20-Sep-1999 #text\_change 20-Jun-2000  
C:Accession: T14554  
R:Viereck, R.  
submitted to the EMBL Data Library, October 1997  
A:Description: Nucleotide sequence from sugar beet calreticulin.  
A:Reference number: Z18137  
A:Accession: T14554  
A:Status: preliminary; translated from GB/EMBL/DBDJ  
A:Molecule type: mRNA  
A:Residues: 1-416 <VIE>  
A:Cross-references: EMBL:AJ02057  
A:Experimental source: strain diploide Inzuchtlinie KWS; leaf  
C:Superfamily: calreticulin  
C:Keywords: calcium binding

Query Match 60.9%; Score 92; DB 2; Length 416;  
Best Local Similarity 63.0%; Pred. No. 1.3e-05;  
Matches 17; Conservative 1; Mismatches 9; Indels 0; Gaps 0;

QY 1 CGPCTKKVHVNIYKGNVLIINKDIRC 27  
Db 143 CGYSTKKVHAIFNIYNDTNHLIKKDVPC 169

Search completed: January 9, 2002, 15:02:03  
Job time: 190 sec

GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: January 9, 2002, 15:12:14 ; Search time 25.18 Seconds  
(without alignments)  
88.823 Million cell updates/sec

Title: US-09-828-000-4  
Perfect score: 340  
Sequence: 1 TDMHGDSEYNMFPGDICGP.....IRCKDDEFTLYTLIVRPDN 61

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 100059 seqs, 36664827 residues

Total number of hits satisfying chosen parameters: 100059

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt\_39:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query %	Match	Length	DB ID	Description
1	340	100.0	417	1	CRTC_HUMAN	P27797 homo sapien
2	335	98.5	400	1	CRTL_BOVIN	P52193 bos taurus
3	335	98.5	416	1	CRTC_MOUSE	P14211 mus musculus
4	335	98.5	416	1	CRTC_RAT	P18418 rattus norv
5	335	98.5	418	1	CRTC_RABIT	P15253 ocyctolagus
6	335	98.5	421	1	CRT2_BOVIN	P42918 bos taurus
7	293	86.2	406	1	CRTC_DRONE	P29413 drosophila
8	261	76.8	388	1	RALL_ONCVO	P11012 onchocerca
9	242	71.2	393	1	CRTC_SCHMA	Q06814 schistosoma
10	233.5	68.7	395	1	CRTC_CAEEL	P27798 caenorhabdi
11	220	64.7	420	1	CRTC_CHLRE	Q9std3 chlamydomon
12	207	60.9	416	1	CRTC_BETVU	O81919 beta vulgar
13	204	60.0	421	1	CRTC_PRUAR	Q9xf98 prunus arme
14	202	59.4	415	1	CRTC_RICCO	P93508 ricinus com
15	202	59.4	424	1	CRT2_ARATH	Q38858 arabidopsis
16	199	58.5	425	1	CRTL_ARATH	O04151 arabidopsis
17	195	57.4	424	1	CRTC_DICDI	O23858 dictyosteli
18	195	57.4	424	1	CRTC_ORVSA	O9slv8 oryza sativ
19	194	57.1	424	1	CRT3_ARATH	O04153 arabidopsis
20	191	56.2	416	1	CRTC_NICPL	Q40401 nicotiana p
21	183	53.8	416	1	CRTC_BERST	Q9zpp1 berberis st
22	177.5	52.2	401	1	CRTC_EUGGR	Q9znp3 euglena gra
23	163	47.9	420	1	CRTC_MAIZE	O9sp22 zea mays (m
24	122.5	36.0	546	1	CALX_SOYEN	Q39817 glycine max
25	121.5	35.7	592	1	CALX_HUMAN	P27824 homo sapien
26	120.5	35.4	591	1	CALX_MOUSE	P35564 mus musculus
27	120.5	35.4	591	1	CALX_RAT	P35565 rattus norv
28	120.5	35.4	593	1	CALX_CANFA	P24643 canis fami
29	115.5	34.0	530	1	CAX1_ARATH	P29402 arabidopsis
30	115.5	34.0	540	1	CALX_HELTU	Q39994 helianthus
31	113.5	34.0	619	1	CALX_CAEEL	P34652 caenorhabdi
32	112.5	33.1	551	1	CALX_PEA	O82709 pisum sativ
33	108.5	31.9	611	1	CALG_MOUSE	P52194 mus musculus

#### RESULT 1

ID	CRTC_HUMAN	STANDARD:	PRT:	417 AA.
AC	P27797;			
DT	01-AUG-1992 (Rel. 23, Created)			
DT	01-AUG-1992 (Rel. 23, Last sequence update)			
DT	20-AUG-2001 (Rel. 40, Last annotation update)			
DE	CALRETICULIN PRECURSOR (CRP55) (CALREGULIN) (HACBP) (ERP60) (52 KDA			
DE	RIBONUCLEOPROTEIN AUTOANTIGEN RO/SS-A).			
GN	CALR OR CRTC.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.			
OX	NCHI_TaxID=9606;			
[1]				
RP	SEQUENCE FROM N.A.			
RP	MEDLINE=92013129; PubMed=1919005;			
RA	Rokeach L.A., Haselby J.A., Mellof J.F., Smeenk R.J., Unnasch T.R.,			
RA	Greene B.M., Hoch S.O.;			
RT	"Characterization of the autoantigen calreticulin.";			
RL	J. Immunol. 147:3031-3039(1991).			
[2]				
RP	SEQUENCE FROM N.A.			
RP	MEDLINE=90237213; PubMed=2332496;			
RA	McCaulliffe D.P., Lux F.A., Lieu T.S., Sanz I., Hanke J., Newkirk M.M.,			
RA	Bachinski L.L., Itoh Y., Siciliano M.J., Reichlin M., Sontheimer R.D.,			
RA	Capra J.D.;			
RT	"Molecular cloning, expression, and chromosome 19 localization of a			
RT	human Ro/SS-A autoantigen.";			
RL	J. Clin. Invest. 85:1379-1391(1990).			
[3]				
RP	SEQUENCE FROM N.A.			
RP	MEDLINE=92129342; PubMed=1733953;			
RA	McCaulliffe D.P., Yang Y.S., Willson J., Sontheimer R.D., Capra J.D.;			
RT	"The 5'-flanking region of the human calreticulin gene shares			
RT	homology with the human GRP78, GRP94, and protein disulfide isomerase			
RT	promoters.";			
RL	J. Biol. Chem. 267:2557-2562(1992).			
[4]				
RP	SEQUENCE FROM N.A.			
RA	Lamerdin J., McCreedy P., Stilwagen S., Ramirez M., Carrano A.;			
RL	Submitted (MAR-1997) to the EMBL/GenBank/DBJ databases.			
[5]				
RP	SEQUENCE OF 18-36.			
RP	MEDLINE=92002034; PubMed=1911778;			
RA	Rojiani M.V., Finlay B.B., Gray V., Dedhar S.;			
RT	"In vitro interaction of a polypeptide homologous to human Ro/SS-A			
RT	antigen (calreticulin) with a highly conserved amino acid sequence in			
RT	the cytoplasmic domain of integrin alpha subunits.";			
RL	Biochemistry 30:9859-9866(1991).			
[6]				
RP	SEQUENCE OF 18-32.			
RP	MEDLINE=90380058; PubMed=2400400;			
RA	Krause K.H., Simmerman H.K.B., Jones L.R., Campbell K.P.;			
RT	"Sequence similarity of calreticulin with a Ca2(+)-binding protein			
RT	that co-purifies with an Ins(1,4,5)P3-sensitive Ca2+ store in HL-60			

34 105.5 31.0 528 1 CAX2\_ARATH Q38798 arabidopsis  
35 103.5 30.4 610 1 CALG\_HUMAN O14967 homo sapien  
36 103 30.3 560 1 CALX\_SCHPO P36581 schizosacch  
37 77.5 22.8 540 1 MTAL\_ACICA P25201 actinobact  
38 66 19.4 560 1 YECO\_YEAST P39994 saccharomyc  
39 64.5 19.0 1766 1 RPBI\_TRYBB P17545 trypanosoma  
40 64.5 19.0 1766 1 RPBI\_TRYBB P17545 trypanosoma  
41 63.5 18.7 489 1 YN98\_YEAST P53755 saccharomyc  
42 63.5 18.7 502 1 CALX\_YEAST P27825 saccharomyc  
43 59 17.4 1361 1 YME9\_YEAST O04693 saccharomyc  
44 58 17.1 286 1 RIPL\_MOMCH P16094 momordica c  
45 58 17.1 496 1 NUSA\_BUCAI P57459 buchnera ap

#### ALIGNMENTS

RT cella.";  
 RL Biochem. J. 270:545-548(1990).  
 [7]  
 RP SKOURNCE OF 18-28.  
 RC TISSUE-Liver;  
 RX MEDLINE-93162045; PubMed 1286669;  
 RA Hochstrasser D.F., Frutiger S., Paquet N., Bairoch A., Ravier F.,  
 RA Pasquali C., Sanchez J.-C., Tissot J.-D., Bjellqvist B., Vargas R.,  
 RA Appel R.D., Hughes G.J.;  
 RT "Human liver protein map: a reference database established by  
 RT microsequencing and gel comparison.";  
 RT Electrophoresis 13:992-1001(1992).  
 [8]  
 RN PARTIAL SEQUENCE OF 25-34; 56-62; 208-221 AND 273-278.  
 RC TISSUE-Keratocytes;  
 RX MEDLINE-93162043; PubMed 1286667;  
 RA Rasmussen H.H., van Damme J., Puype M., Gesser B., Celis J.E.,  
 RA Vandekerckhove J.;  
 RT "Microsequences of 145 proteins recorded in the two-dimensional gel  
 RT protein database of normal human epidermal keratinocytes.";  
 RL Electrophoresis 13:960-969(1992).  
 [9]  
 RN SEQUENCE OF 18-26.  
 RC TISSUE-Colon carcinoma;  
 RX MEDLINE-97295306; PubMed-9150948;  
 RA Ji H., Reid G.E., Moritz R.L., Eddes J.S., Burgess A.W., Simpson R.J.;  
 RT "A two-dimensional gel database of human colon carcinoma proteins.";  
 RL Electrophoresis 18:605-613(1997).  
 CC -|- FUNCTION: THIS PROTEIN BINDS CALCIUM. THERE ARE BOTH HIGH AND  
 CC LOW AFFINITY CALCIUM-BINDING SITES.  
 CC -|- SUBUNIT: MONOMER (BY SIMILARITY).  
 CC -|- SUBCELLULAR LOCATION: ENDOPLASMIC RETICULUM LUMEN.  
 CC -|- SIMILARITY: BELONGS TO THE CALRETICULIN FAMILY.  
 CC -|- CAUTION: WAS ORIGINALLY (REF.2) THOUGHT TO BE THE RO AUTOANTIGEN.  
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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 [10]  
 DR EMBL; M84739; AAA51916.1; -;  
 DR EMBL; M32294; AAA36582.1; -;  
 DR EMBL; AD000092; AAB51176.1; -;  
 DR PIR; A37047; A37047.  
 DR PIR; S11475; S11475.  
 DR PIR; A42330; A42330.  
 DR PIR; A46452; A46452.  
 DR SWISS-2DPAGE; P27797; HUMAN.  
 DR Aurbus/Ghent-2DPAGE; 9401; IEF.  
 DR HSC-2DPAGE; P27797; HUMAN.  
 DR NIM; 109091; -;  
 DR InterPro; IPR001580; Calreticulin.  
 DR Pfam; PF00262; calreticulin; 1.  
 DR PRINTS; PR00626; CALRETICULIN.  
 DR PRODOM; PD001866; Calreticulin; 1.  
 DR PROSITE; PS00014; ER-TARGET; 1.  
 DR PROSITE; PS00803; CALRETICULIN\_1; 1.  
 DR PROSITE; PS00804; CALRETICULIN\_2; 1.  
 DR PROSITE; PS00805; CALRETICULIN\_REPEAT; 3.  
 KW Endoplasmic reticulum; Calcium-binding; Repeat; Signal.  
 FT SIGNAL 1 17  
 FT CHAIN 18 417 CALRETICULIN.  
 FT DOMAIN 18 197 N-DOMAIN.  
 FT DOMAIN 198 308 P-DOMAIN.  
 FT DOMAIN 309 417 C-DOMAIN.  
 FT DOMAIN 191 255 4 X APPROXIMATE REPEATS.  
 FT REPEAT 191 202 1-1.  
 FT REPEAT 210 221 1-2.  
 FT REPEAT 227 238 1-3.

FT REPEAT 244 255 1-4.  
 FT DOMAIN 259 297 3 X APPROXIMATE REPEATS.  
 FT REPEAT 259 283 2-1.  
 FT REPEAT 273 283 2-2.  
 FT REPEAT 287 297 2-3.  
 FT DOMAIN 351 408 ASP/GLU/LYS-RICH.  
 FT DISULFID 137 163 BY SIMILARITY.  
 FT SITE 414 417 PREVENT SECRETION FROM ER.  
 FT CONFLICT 35 35 MISSING (IN REF. 3).  
 SQ SEQUENCE 417 AA; 48141 MW; BC37C3C0F1054FB2 CRC64;  
 Query Match 100.0%; Score 340; DB 1; Length 417;  
 Best Local Similarity 100.0%; Pred. No. 3.4e-34; Indels 0; Gaps 0;  
 Matches 61; Conservative 0; Mismatches 0;  
 QY 1 TDMHGDSYNIAMFGPDICGPGTKKVVHVIYFKGKNNVINKDKRDKDETHLYTLIVRPD 60  
 Db 120 TDMHGDSYNIAMFGPDICGPGTKKVVHVIYFKGKNNVINKDKRDKDETHLYTLIVRPD 179  
 QY 61 N 61  
 Db 180 N 180  
 RESULT 2  
 CRTL\_BOVIN  
 ID CRTL\_BOVIN STANDARD; PRT: 400 AA.  
 AC P52193;  
 DT 01-OCT-1996 (Rel. 34, Created)  
 DT 01-OCT-1996 (Rel. 34, Last sequence update)  
 DT 01-OCT-1996 (Rel. 34, Last annotation update)  
 DE CALRETICULIN, BRAIN ISOFORM 1 (CRP55) (CALREGULIN) (HACBP).  
 OS Bos taurus (Bovine).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
 OC Bovidae; Bovinae; Bos.  
 OX NCBI\_TaxID-9913;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE-Brain;  
 RX MEDLINE-94183174; PubMed-8135753;  
 RA Matsuoka K., Seta K., Yamakawa Y., Okuyama T., Shinoda T., Isobe T.;  
 RL "Covalent structure of bovine brain calreticulin.";  
 RL Biochem. J. 298:435-442(1994).  
 CC -|- FUNCTION: THIS PROTEIN BINDS CALCIUM. THERE ARE BOTH HIGH AND  
 CC LOW AFFINITY CALCIUM-BINDING SITES.  
 CC -|- SUBUNIT: MONOMER.  
 CC -|- SUBCELLULAR LOCATION: ENDOPLASMIC RETICULUM LUMEN.  
 CC -|- SIMILARITY: BELONGS TO THE CALRETICULIN FAMILY.  
 DR InterPro; IPR001580; Calreticulin.  
 DR Pfam; PF00262; calreticulin; 1.  
 DR PRINTS; PR00626; CALRETICULIN.  
 DR PRODOM; PD001866; Calreticulin; 1.  
 DR PROSITE; PS00014; ER-TARGET; 1.  
 DR PROSITE; PS00803; CALRETICULIN\_1; 1.  
 DR PROSITE; PS00804; CALRETICULIN\_2; 1.  
 DR PROSITE; PS00805; CALRETICULIN\_REPEAT; 3.  
 KW Endoplasmic reticulum; Calcium-binding; Repeat; Glycoprotein.  
 FT DOMAIN 1 180 N-DOMAIN.  
 FT DOMAIN 181 291 P-DOMAIN.  
 FT DOMAIN 292 400 C-DOMAIN.  
 FT DOMAIN 174 238 4 X APPROXIMATE REPEATS.  
 FT REPEAT 174 185 1-1.  
 FT REPEAT 193 204 1-2.  
 FT REPEAT 210 221 1-3.  
 FT REPEAT 227 238 1-4.  
 FT DOMAIN 242 280 3 X APPROXIMATE REPEATS.  
 FT REPEAT 242 252 2-1.  
 FT REPEAT 256 266 2-2.  
 FT REPEAT 270 280 2-3.  
 FT DOMAIN 334 390 ASP/GLU/LYS-RICH.

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FT DISULFID 120 146
FT CARBOHYD 162 162
FT SITE 397 400
SQ SEQUENCE 400 AA: 46381 MW; 7D4B68DFC689EEF1 CRC64;

Query Match 98.5%; Score 335; DB 1; Length 400;
Best Local Similarity 98.4%; Pred. No. 1.3e-33;
Matches 60; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TMHGDSEYNIMFGPDICGPGTKKHVIFNYGKGNVLINKDIRCKDDETHLYTLIVRPD 60
DB 103 TMHGDSEYNIMFGPDICGPGTKKHVIFNYGKGNVLINKDIRCKDDETHLYTLIVRPD 162

QY 61 N 61
DB 163 N 163

RESULT 3
CRTC_MOUSE STANDARD; PRT; 416 AA.
AC P14211;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE CALRETICULIN PRECURSOR (CRP55) (CALREGULIN) (HACBP) (ERP60).
GN CALR.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 18-48 AND 129-161.
RC STRAIN=BALB/C; TISSUE=Liver;
RX MEDLINE=90059955; PubMed=2583110;
RA Smith M.J., Koch G.L.E.;
RT "Multiple zones in the sequence of calreticulin (CRP55, calregulin, HACBP), a major calcium binding ER/SR protein.";
RL EMBO J. 8:3581-3586(1989).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=93013037; PubMed=1398135;
RA Mazzarella R.A., Gold P., Cunningham M., Green M.;
RT "Determination of the sequence of an expressible cDNA clone encoding ERp60/calregulin by the use of a novel nested set method.";
RL Gene 120:217-225(1992).
RN [3]
RP SEQUENCE OF 18-38.
RC TISSUE=Fibroblast;
RX MEDLINE=95009907; PubMed=7523108;
RA Merrick B.A., Patterson R.M., Wichter L.L., He C., Selkirk J.K.;
RT "Separation and sequencing of familial and novel murine proteins using preparative two-dimensional gel electrophoresis.";
RL Electrophoresis 15:735-745(1994).
CC -!- FUNCTION: THIS PROTEIN BINDS CALCIUM. THERE ARE BOTH HIGH AND LOW AFFINITY CALCIUM-BINDING SITES.
CC -!- SUBUNIT: MONOMER (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: ENDOPLASMIC RETICULUM LUMEN.
CC -!- SIMILARITY: BELONGS TO THE CALRETICULIN FAMILY.
CC -----
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CC -----
DR EMBL; X14926; CAA33053.1; -
DR EMBL; M92988; AAA37569.1; -
DR PIR; S06763; S06763.
DR PIR; JC1444; JC1444.
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DR SWISS-2DPAGE; P14211; MOUSE.
DR MGD; MGI:88252; Calr.
DR InterPro; IPR001580; Calreticulin.
DR InterPro; IPR000886; ER_target.
DR Pfam; PF00262; calreticulin; 1.
DR PRINTS; PR00626; CALRETICULIN.
DR PRODOM; PD001866; Calreticulin; 1.
DR PROSITE; PS00014; ER_TARGET; 1.
DR PROSITE; PS00803; CALRETICULIN_1; 1.
DR PROSITE; PS00804; CALRETICULIN_2; 1.
DR PROSITE; PS00805; CALRETICULIN_REPEAT; 3.
KW Endoplasmic reticulum; Calcium-binding; Repeat; Signal.
FT SIGNAL 1 17
FT CHAIN 18 416 CALRETICULIN.
FT DOMAIN 18 197 N-DOMAIN.
FT DOMAIN 198 308 P-DOMAIN.
FT DOMAIN 309 416 C-DOMAIN.
FT DOMAIN 191 255 4 X APPROXIMATE REPEATS.
FT REPEAT 191 202 1-1.
FT REPEAT 210 221 1-2.
FT REPEAT 227 238 1-3.
FT REPEAT 244 255 1-4.
FT DOMAIN 259 297 3 X APPROXIMATE REPEATS.
FT REPEAT 259 269 2-1.
FT REPEAT 273 283 2-2.
FT REPEAT 287 297 2-3.
FT DOMAIN 351 407 ASP/GLU/LYS-RICH.
FT DISULFID 137 163 BY SIMILARITY.
FT SITE 413 416 PREVENT SECRETION FROM ER.
SQ SEQUENCE 416 AA: 47994 MW; 24C03B00913408D8 CRC64;

Query Match 98.5%; Score 335; DB 1; Length 416;
Best Local Similarity 100.0%; Pred. No. 1.4e-33;
Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DMHGDSEYNIMFGPDICGPGTKKHVIFNYGKGNVLINKDIRCKDDETHLYTLIVRPD 61
DB 121 DMHGDSEYNIMFGPDICGPGTKKHVIFNYGKGNVLINKDIRCKDDETHLYTLIVRPD 180

RESULT 4
CRTC_MOUSE STANDARD; PRT; 416 AA.
AC P18418; P10452;
DT 01-MAR-1989 (Rel. 10, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE CALRETICULIN PRECURSOR (CRP55) (CALREGULIN) (HACBP) (ERP60) (CALBP) (CALR).
GN CALR.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SPRAGUE-DAWLEY; TISSUE=Brain cortex;
RX MEDLINE=90370496; PubMed=2395661;
RA Murthy K.K., Banville D., Srikanth C.B., Carrier F., Bell A., Holmes C., Patel Y.C.;
RT "Structural homology between the rat calreticulin gene product and the Onchocerca volvulus antigen Rat-1.";
RL Nucleic Acids Res. 18:4933-4933(1990).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=SPRAGUE-DAWLEY;
RX MEDLINE=93202172; PubMed=8453984;
RA Nakamura M., Moriya M., Baba T., Michikawa Y., Yamanobe T., Arai K., Okinaga S., Kobayashi T.;
RT "An endoplasmic reticulum protein, calreticulin, is transported into the acrosome of rat sperm.";
RL Exp. Cell Res. 205:101-110(1993).
```

[3] SEQUENCE FROM N.A.  
 RP STRAIN SPRAGUE-DAWLEY; TISSUE: Liver;  
 RX MEDLINE-95181573; PubMed-7876339;  
 RA Sennichsen B., Fliedek J., van Nguyen P., Diekmann W.,  
 RA Robinson D.G., Fieskes G.;  
 RT "Retention and retrieval: both mechanisms cooperate to maintain  
 RT calreticulin in the endoplasmic reticulum.";  
 RL J. Cell Sci. 107:2705-2717(1994).  
 [4] SEQUENCE OF 270-358 FROM N.A.  
 RP STRAIN SPRAGUE-DAWLEY;  
 RA Lone Y.C., Bailey A., Latruffe N.;  
 RL Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.  
 [5] SEQUENCE OF 18-29.  
 RP MEDLINE-91054414; PubMed-2241926;  
 RX Treves S., de Mattei M., Lanfredi M., Villa A., Green N.M.,  
 RA MacLennan D.H., Meldolesi J., Pozzan T.;  
 RT "Calreticulin is a candidate for a calsequestrin-like function in  
 RT Ca2(+)-storage compartments (calciosomes) of liver and brain.";  
 RL Biochem. J. 271:473-480(1990).  
 [6] SEQUENCE OF 18-32.  
 RP STRAIN SPRAGUE-DAWLEY; TISSUE: Testis;  
 RX MEDLINE-92360010; PubMed-1497655;  
 RA Nakamura M., Michikawa Y., Baba T., Okinaga S., Arai K.;  
 RT "Calreticulin is present in the acrosome of spermatids of rat  
 RT testis.";  
 RL Biochem. Biophys. Res. Commun. 186:668-673(1992).  
 [7] SEQUENCE OF 18-32.  
 RP STRAIN LEC; TISSUE: Liver;  
 RX MEDLINE-94072621; PubMed-8251535;  
 RA Yokoi T., Nagayama S., Kajiwara R., Kawaguchi Y., Horiuchi R.,  
 RA Kametaki T.;  
 RT "Identification of protein disulfide isomerase and calreticulin as  
 RT autoantigen antigens in LEC strain of rats.";  
 RL Biochim. Biophys. Acta 1158:339-344(1993).  
 CC -1- FUNCTION: THIS PROTEIN BINDS CALCIUM. THERE ARE BOTH HIGH AND  
 CC LOW AFFINITY CALCIUM-BINDING SITES.  
 CC -1- SUBUNIT: MONOMER (BY SIMILARITY).  
 CC -1- SUBCELLULAR LOCATION: ENDOPLASMIC RETICULUM LUMEN.  
 CC -1- SIMILARITY: BELONGS TO THE CALRETICULIN FAMILY.  
 CC -1- CAUTION: WAS ORIGINALLY (REF.2) THOUGHT TO BE D-BETA-  
 CC HYDROXYBUTYRATE DEHYDROGENASE.  
 -----  
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 DR EMBL: D78308; BAAL1345.1; -;  
 DR EMBL: X53363; CAA37446.1; -;  
 DR EMBL: X13702; CAA31987.1; ALT\_SEQ.  
 DR EMBL: X79347; CAA55890.1; -;  
 DR PIR: S04867; S04867.  
 DR PIR: S11205; S11205.  
 DR PIR: S13045; S13045.  
 DR PIR: A49176; A49176.  
 DR PIR: S45036; S45036.  
 DR PIR: JH0819; JH0819.  
 DR InterPro: IPR001580; Calreticulin.  
 DR InterPro: IPR000886; ER target.  
 DR Pfam: PF00262; calreticulin; 1.  
 DR PRINTS: PR00626; CALRETICULIN.  
 DR ProDom: PD001866; Calreticulin; 1.  
 DR PROSITE: PS00014; ER\_TARGET; 1.  
 DR PROSITE: PS00803; CALRETICULIN\_1; 1.  
 DR PROSITE: PS00804; CALRETICULIN\_2; 1.

DR PROSITE: PS00805; CALRETICULIN\_REPEAT; 3.  
 KW Endoplasmic reticulum; Calcium-binding; Repeat; Signal.  
 FT SIGNAL 1 17  
 FT CHAIN 18 416 CALRETICULIN.  
 FT DOMAIN 18 197 N-DOMAIN.  
 FT DOMAIN 198 308 P-DOMAIN.  
 FT DOMAIN 309 416 C-DOMAIN.  
 FT DOMAIN 191 255 4 X APPROXIMATE REPEATS.  
 FT REPEAT 191 202 1-1.  
 FT REPEAT 210 221 1-2.  
 FT REPEAT 227 238 1-3.  
 FT REPEAT 244 255 1-4.  
 FT DOMAIN 259 297 3 X APPROXIMATE REPEATS.  
 FT REPEAT 273 283 2-1.  
 FT REPEAT 287 297 2-2.  
 FT REPEAT 351 407 ASP/GLU/LYS-RICH.  
 FT DOMAIN 137 163 BY SIMILARITY.  
 FT DISULFID 413 416 PREVENT SECRETION FROM ER.  
 FT SITE 416  
 SQ SEQUENCE 416 AA; 47995 MW; 2E6713CED31A2970 CRC64;  
 Query Match 98.5%; Score 335; DB 1; Length 416;  
 Best Local Similarity 100.0%; Pred. No. 1.4e-33;  
 Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 2 DMHGSEYNIMFGPDICGPGTKKVVHVFNYKGNVINKDKDDEFTHLYTLIVRPD 61  
 DB 121 DMHGSEYNIMFGPDICGPGTKKVVHVFNYKGNVINKDKDDEFTHLYTLIVRPD 180  
 RESULT 5  
 CRIC\_RABIT STANDARD; PRT; 418 AA.  
 ID CRIC\_RABIT AC P15253;  
 DT 01-APR-1990 (Rel. 14, Created)  
 DT 01-APR-1990 (Rel. 14, Last sequence update)  
 DT 01-OCT-1996 (Rel. 34, Last annotation update)  
 DE CALRETICULIN PRECURSOR (CRP55) (CALREGULIN) (HACBP) (BRP60).  
 GN CALR.  
 OS Oryctolagus cuniculus (Rabbit).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.  
 OX NCBI\_TaxID:9986;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE:slow-twitch skeletal muscle;  
 RX MEDLINE-90094320; PubMed-2600080;  
 RA Fliegel L., Burns K., MacLennan D.H., Reithmeier R.A.F., Michalak M.;  
 RT "Molecular cloning of the high affinity calcium-binding protein  
 RT (calreticulin) of skeletal muscle sarcoplasmic reticulum.";  
 RL J. Biol. Chem. 264:21522-21528(1989).  
 [2] SEQUENCE FROM N.A.  
 RP TISSUE:Fast-twitch skeletal muscle;  
 RX MEDLINE-91282795; PubMed-2059224;  
 RA Fliegel L., Michalak M.;  
 RT "Fast-twitch and slow-twitch skeletal muscles express the same  
 RT isoform of calreticulin.";  
 RL Biochem. Biophys. Res. Commun. 177:979-984(1991).  
 [3] SEQUENCE OF 18-36.  
 RX MEDLINE-91054414; PubMed-2241926;  
 RA Treves S., de Mattei M., Lanfredi M., Villa A., Green N.M.,  
 RA MacLennan D.H., Meldolesi J., Pozzan T.;  
 RT "Calreticulin is a candidate for a calsequestrin-like function in  
 RT Ca2(+)-storage compartments (calciosomes) of liver and brain.";  
 RL Biochem. J. 271:473-480(1990).  
 [4] SEQUENCE OF 18-46.  
 RP MEDLINE-91201375; PubMed-2016321;  
 RA Milner R.E., Baksh S., Shemanko C., Carpenter M.R., Smillie L.,  
 RA Vance J.E., Opas M., Michalak M.;

RT "Calreticulin, and not calsequestrin, is the major calcium binding  
 RT protein of smooth muscle sarcoplasmic reticulum and liver endoplasmic  
 RL reticulum.";  
 RL J. Biol. Chem. 266:7155-7165(1991).  
 RN [5]  
 RP PARTIAL SEQUENCE.  
 RC TISSUE=Lung;  
 RX MEDLINE=92002038; PubMed=1911780;  
 RA Guan S., Fallick A.M., Williams D.E., Cashman J.R.;  
 RT "Evidence for complex formation between rabbit lung flavin-containing  
 RT monooxygenase and calreticulin.";  
 RL Biochemistry 30:9892-9900(1991).  
 CC Biochemistry 30:9892-9900(1991).  
 CC -!- FUNCTION: THIS PROTEIN BINDS CALCIUM. THERE ARE BOTH HIGH AND  
 CC LOW AFFINITY CALCIUM-BINDING SITES.  
 CC -!- SUBUNIT: MONOMER (BY SIMILARITY).  
 CC -!- SUBCELLULAR LOCATION: ENDOPLASMIC RETICULUM LUMEN.  
 CC -!- SIMILARITY: BELONGS TO THE CALRETICULIN FAMILY.  
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 CC -----  
 DR EMBL; J05138; AAA31188.1; -;  
 DR PIR; A34154; A34154.  
 DR PIR; C33208; C33208.  
 DR PIR; D33208; D33208.  
 DR PIR; E33208; E33208.  
 DR PIR; F33208; F33208.  
 DR PIR; S13046; S13046.  
 DR PIR; S13047; S13047.  
 DR InterPro; IPR001580; Calreticulin.  
 DR InterPro; IPR000886; ER.target.  
 DR Pfam; PF00262; calreticulin; 1.  
 DR PRODOM; PD001866; CALRETICULIN; 1.  
 DR PROSITE; PS00014; ER.TARGET; 1.  
 DR PROSITE; PS00803; CALRETICULIN\_1; 1.  
 DR PROSITE; PS00804; CALRETICULIN\_2; 1.  
 DR PROSITE; PS00805; CALRETICULIN\_REPEAT; 3.  
 KW Endoplasmic reticulum; Calcium-binding; Repeat; Signal.  
 FT SIGNAL 1 17  
 FT CHAIN 18 418 CALRETICULIN.  
 FT DOMAIN 18 197 N-DOMAIN.  
 FT DOMAIN 198 308 P-DOMAIN.  
 FT DOMAIN 309 418 C-DOMAIN.  
 FT REPEAT 191 255 4 X APPROXIMATE REPEATS.  
 FT REPEAT 210 221 1-1.  
 FT REPEAT 210 221 1-2.  
 FT REPEAT 227 238 1-3.  
 FT REPEAT 244 255 1-4.  
 FT DOMAIN 259 297 3 X APPROXIMATE REPEATS.  
 FT REPEAT 259 269 2-1.  
 FT REPEAT 273 283 2-2.  
 FT REPEAT 287 297 2-3.  
 FT DOMAIN 351 408 ASP/GLU/LYS-RICH.  
 FT DISULFID 137 163 BY SIMILARITY.  
 FT SITE 415 418 PREVENT SECRETION FROM ER.  
 FT VARIANT 35 35 E -> D.  
 FT CONFLICT 90 90 P -> T (IN REF. 5).  
 SQ SEQUENCE 418 AA; 48275 MW; B6082B689DC763A6 CRC64;

Query Match 98.5%; Score 335; DB 1; Length 418;  
 Best Local Similarity 100.0%; Pred. No. 1.4e-33;  
 Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DMHGDSEYNIMFGPDICGPGTKKVVHIFNYKGNVLINKDIRCKDDEFFHLYTLIVRPDN 61  
 |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 DB 121 DMHGDSEYNIMFGPDICGPGTKKVVHIFNYKGNVLINKDIRCKDDEFFHLYTLIVRPDN 180

RESULT 6  
 CRT2\_BOVIN STANDARD; PRT; 421 AA.  
 ID CRT2\_BOVIN  
 AC P42918;  
 DT 01-NOV-1995 (Rel. 32, Created)  
 DT 01-NOV-1995 (Rel. 32, Last sequence update)  
 DE 15-JUL-1998 (Rel. 36, Last annotation update)  
 DE CALRETICULIN, BRAIN ISOFORM 2 PRECURSOR (CRP55) (CALREGULIN) (HACBP).  
 OS Bos taurus (Bovine).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
 OC Bovidae; Bovinae; Bos.  
 OX NCBI\_TaxID=9913;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Brain;  
 RX MEDLINE=93385184; PubMed=8373827;  
 RA Liu N., Fine R.E., Johnson R.J.;  
 RT "Comparison of cDNAs from bovine brain coding for two isoforms of  
 RT calreticulin.";  
 RL Biochim. Biophys. Acta 1202:70-76(1993).  
 CC -!- FUNCTION: THIS PROTEIN BINDS CALCIUM. THERE ARE BOTH HIGH AND  
 CC LOW AFFINITY CALCIUM-BINDING SITES.  
 CC -!- SUBUNIT: MONOMER (BY SIMILARITY).  
 CC -!- SUBCELLULAR LOCATION: ENDOPLASMIC RETICULUM LUMEN.  
 CC -!- SIMILARITY: BELONGS TO THE CALRETICULIN FAMILY.  
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 CC -----  
 DR EMBL; L13462; AAC37307.1; -;  
 DR InterPro; IPR001580; Calreticulin.  
 DR InterPro; IPR000886; ER.target.  
 DR Pfam; PF00262; calreticulin; 1.  
 DR PRINTS; PR00626; CALRETICULIN.  
 DR PRODOM; PD001866; Calreticulin; 1.  
 DR PROSITE; PS00014; ER.TARGET; 1.  
 DR PROSITE; PS00803; CALRETICULIN\_1; 1.  
 DR PROSITE; PS00804; CALRETICULIN\_2; 1.  
 DR PROSITE; PS00805; CALRETICULIN\_REPEAT; 3.  
 KW Endoplasmic reticulum; Calcium-binding; Repeat; Signal.  
 FT SIGNAL 1 34 POTENTIAL.  
 FT CHAIN 35 421 CALRETICULIN, BRAIN ISOFORM 2.  
 FT DOMAIN 35 201 N-DOMAIN.  
 FT DOMAIN 202 312 P-DOMAIN.  
 FT DOMAIN 313 421 C-DOMAIN.  
 FT DOMAIN 195 259 4 X APPROXIMATE REPEATS.  
 FT REPEAT 214 225 1-1.  
 FT REPEAT 231 242 1-2.  
 FT REPEAT 248 259 1-3.  
 FT REPEAT 263 301 1-4.  
 FT DOMAIN 263 301 3 X APPROXIMATE REPEATS.  
 FT REPEAT 263 273 2-1.  
 FT REPEAT 277 287 2-2.  
 FT REPEAT 291 301 2-3.  
 FT DOMAIN 366 411 ASP/GLU/LYS-RICH.  
 FT DISULFID 141 167 BY SIMILARITY.  
 FT CARBOHYD 183 183 N-LINKED (GLCNAC. .) (POTENTIAL).  
 FT SITE 421 PREVENT SECRETION FROM ER.  
 SQ SEQUENCE 421 AA; 48812 MW; 0257E959F71528BC CRC64;

Query Match 98.5%; Score 335; DB 1; Length 421;  
 Best Local Similarity 98.4%; Pred. No. 1.4e-33;  
 Matches 60; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TDMHGDSEYNIMFGPDICGPTGKVKHVIFNYKGNVLINKIRCKDDETHLYTLVRPD 60  
 DB 124 TDMHGDSEYNIMFGPDICGPTGKVKHVIFNYKGNVLINKIRCKDDETHLYTLVRPN 183  
 QY 61 N 61  
 DB 184 N 184

RESULT 7  
 CMTCDROME STANDARD; PRT; 406 AA.  
 AC P29413; Q9VHA3;  
 DT 01-APR-1993 (Rel. 25, Created)  
 DT 01-OCT-1993 (Rel. 27, Last sequence update)  
 DT 20-AUG-2001 (Rel. 40, Last annotation update)  
 DE CALRETICULIN PRECURSOR (CRP55) (CALREGULIN) (HACBP).  
 GN CRC OR CG9429.  
 OS Drosophila melanogaster (Fruit fly).  
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;  
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
 OC Ephydroidea; Drosophilidae; Drosophila.  
 OX NCBI\_TaxID:7227;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE-93208374; PubMed-1296819;  
 RA Smith M.J.;  
 RT "Nucleotide sequence of a Drosophila melanogaster gene encoding a  
 calreticulin homologue.";  
 RL DNA Seq. 3:247-250(1992).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN BERKELEY;  
 RX MEDLINE-20196006; PubMed-10731132;  
 RA Adams M.D., Celisner S.E., Holt R.A., Evans C.A., Gocayne J.D.,  
 RA Amaratunga P.G., Scherer S.E., Li P.W., Hoskins R.A., Galie R.F.,  
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,  
 RA Sutton G.G., Wortman J.R., Vandeil M.D., Zhang Q., Chen L.X.,  
 RA Brandon R.C., Rogers J.H.C., Blazer R.G., Champe M., Pfeiffer B.D.,  
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,  
 RA Buller R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,  
 RA Abell J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,  
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,  
 RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,  
 RA Burris K.C., Busam D.A., Butler H., Cadiou E., Center A., Chandra I.,  
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,  
 RA de Pablos B., Delecher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,  
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,  
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,  
 RA Foster C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,  
 RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,  
 RA Harris N.L., Harvey D., Holman T.J., Hernandez J.R., Houck J.,  
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,  
 RA Julali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,  
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,  
 RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,  
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,  
 RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,  
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,  
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacle J.M.,  
 RA Paluzzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,  
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,  
 RA Shue B.C., Siden-Kimons I., Simpson M., Skupski M.P., Smith T.,  
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,  
 RA Swirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,  
 RA Wang Z.-Y., Wasserman D.A., Weissstock G.M., Weissbach J.,  
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,  
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,  
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu H.O.,  
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;  
 RT "The genome sequence of Drosophila melanogaster.";  
 RL Science 287:2185-2195(2000).  
 RN [3]

RP SEQUENCE OF 91-124 AND 182-220.  
 RX MEDLINE-90307981; PubMed-2365822;  
 RA McCaulliffe D.P., Zappi E., Lieu T.S., Michalak M., Sontheimer R.D.,  
 RA Capra J.D.;  
 RT "A human Ro/SS-A autoantigen is the homologue of calreticulin and is  
 RT highly homologous with oncohercal RAL-1 antigen and an aplysia  
 RT 'memory molecule'.";  
 RL J. Clin. Invest. 86:332-335(1990).  
 CC -!- FUNCTION: THIS PROTEIN BINDS CALCIUM. THERE ARE BOTH HIGH AND  
 CC LOW AFFINITY CALCIUM-BINDING SITES.  
 CC -!- SUBCELLULAR LOCATION: ENDOPLASMIC RETICULUM LUMEN.  
 CC -!- SIMILARITY: BELONGS TO THE CALRETICULIN FAMILY.  
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 DR EMBL; X64461; CAA45791.1; -  
 DR EMBL; AE003683; AAF54416.1; -  
 DR PIR; A37158; A37158.  
 DR FlyBase; FBgn0005585; Crc.  
 DR InterPro; IPR001580; Calreticulin.  
 DR InterPro; IPR000896; ER\_target.  
 DR Pfam; PF00262; calreticulin; 1.  
 DR PRINTS; PR00626; CALRETICULIN.  
 DR ProDom; PD001866; Calreticulin; 1.  
 DR PROSITE; PS00014; ER\_TARGET; 1.  
 DR PROSITE; PS00803; CALRETICULIN\_1; 1.  
 DR PROSITE; PS00804; CALRETICULIN\_2; 1.  
 DR PROSITE; PS00805; CALRETICULIN\_REPEAT; 3.  
 KW Endoplasmic reticulum; Calcium-binding; Repeat; Signal.  
 FT SIGNAL 18 17 POTENTIAL.  
 FT CHAIN 18 406 CALRETICULIN.  
 FT CONFLICT 107 107 G -> A (IN REF. 3).  
 FT CONFLICT 184 184 V -> L (IN REF. 3).  
 SQ SEQUENCE 406 AA; 46808 MW; 65D72C69D0BEC427 CRC64;  
 Query Match 86.2%; Score 293; DB 1; Length 406;  
 Best Local Similarity 85.2%; Pred. No. 1.8e-28;  
 Matches 52; Conservative 4; Mismatches 5; Indels 0; Gaps 0;  
 QY 1 TDMHGDSEYNIMFGPDICGPTGKVKHVIFNYKGNVLINKIRCKDDETHLYTLVRPD 60  
 DB 120 TDMHGDSEYNIMFGPDICGPTGKVKHVIFNYKGNVLINKIRCKDDETHLYTLVRPD 179  
 QY 61 N 61  
 DB 180 N 180

RESULT 8  
 RALLONCVO STANDARD; PRT; 388 AA.  
 ID RALLONCVO  
 AC P11012;  
 DT 01-JUL-1989 (Rel. 11, Created)  
 DT 01-NOV-1995 (Rel. 32, Last sequence update)  
 DT 01-OCT-1996 (Rel. 34, Last annotation update)  
 DE RAL-1 PROTEIN PRECURSOR (41 KDA LARVAL ANTIGEN).  
 GN RALI.  
 OS Onchocerca volvulus.  
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Spirurida; Filarioidea;  
 OC Onchocercidae; Onchocerca.  
 OX NCBI\_TaxID:6282;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE-94341871; PubMed-7520419;  
 RA Rokeach L.A., Zimmerman P.A., Unnasch T.R.;  
 RT "Epitopes of the Onchocerca volvulus RALI antigen, a member of the





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AC Q9STD3;
DT 20-AUG-2001 (Rel. 40, Created)
DT 20-AUG-2001 (Rel. 40, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE CALRETICULIN PRECURSOR.
OS Chlamydomonas reinhardtii.
OC Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;
OC Chlamydomonadaceae; Chlamydomonas.
ON NCBI_TaxID=3055;
RX [1]
RP SEQUENCE FROM N.A.
RC STRAIN=137C;
RA Zuppin A., Kaydamov C.;
RT "Cloning and characterization of a cDNA encoding Chlamydomonas
RL reinhardtii calreticulin.";
CC -1- FUNCTION: THIS PROTEIN BINDS CALCIUM. THERE ARE BOTH HIGH AND
CC LOW AFFINITY CALCIUM-BINDING SITES (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: ENDOPLASMIC RETICULUM LUMEN (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE CALRETICULIN FAMILY.
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CC -----
DR EMBL; AJ000765; CAB54526.1; -.
DR InterPro; IPR001580; Calreticulin.
DR InterPro; IPR000886; ER_target.
DR Pfam; PF00262; calreticulin; 1.
DR PRINTS; PR00626; CALRETICULIN.
DR PRODOM; PD001866; Calreticulin; 1.
DR PROSITE; PS00014; ER_TARGET; 1.
DR PROSITE; PS00803; CALRETICULIN_1; 1.
DR PROSITE; PS00804; CALRETICULIN_2; 1.
DR PROSITE; PS00805; CALRETICULIN_REPEAT; 1.
DR Endoplasmic reticulum; Calcium-binding; Repeat; Signal.
KW SIGNAL
FT SIGNAL 1 18 POTENTIAL.
FT CHAIN 19 420 CALRETICULIN.
FT SITE 417 420 PREVENT SECRETION FROM ER (POTENTIAL).
FT SITE 420 420 DD3BA3AFBF61C9B CRC64;
SQ SEQUENCE 420 AA; 47327 MW;
Query Match 64.7%; Score 220; DB 1; Length 420;
Best Local Similarity 64.9%; Pred.No.1.5e-19;
Matches 37; Conservative 10; Mismatches 10; Indels 0; Gaps 0;
QY 5 GDSYNYMFGPDICGPTKKVHVHVFYKGNVLNKDIRCKDDETHLYTLIVRPDN 61
||: ||:||||||| 1:|||| ||||| || ||||: ||: ||:||||:|
Db 127 GDTPYSMFGPDICGYSTRKVVHVLTYKGNKYLKKDKAETDQLTHVTVLIVRPDN 183
RESULT 12
CRTC_BETVU
ID CRTC_BETVU STANDARD; PRT; 416 AA.
AC O81919;
DT 20-AUG-2001 (Rel. 40, Created)
DT 20-AUG-2001 (Rel. 40, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE CALRETICULIN PRECURSOR.
OS Beta vulgaris (sugar beet).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Caryophyllidae; Caryophyllales; Chenopodiaceae; Beta.
ON NCBI_TaxID=3555;
RX [1]
RP SEQUENCE FROM N.A.
RC STRAIN=VV-D/2R5; TISSUE=Leaf;
RA Vliereck R.;
RT "Nucleotide sequence from sugar beet calreticulin.";
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RL Submitted (OCT-1997) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: THIS PROTEIN BINDS CALCIUM. THERE ARE BOTH HIGH AND
CC LOW AFFINITY CALCIUM-BINDING SITES (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: ENDOPLASMIC RETICULUM LUMEN (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE CALRETICULIN FAMILY.
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CC -----
DR EMBL; AJ002057; CAA05161.1; -
DR Mendel; 32549; Betvu:1166; 32549.
DR InterPro; IPR001580; Calreticulin.
DR InterPro; IPR000886; ER.target.
DR Pfam; PF00262; calreticulin; 1.
DR PRINTS; PR00626; CALRETICULIN.
DR ProDom; PD001866; Calreticulin; 1.
DR PROSITE; PS00014; ER_TARGET; 1.
DR PROSITE; PS00803; CALRETICULIN_1; 1.
DR PROSITE; PS00804; CALRETICULIN_2; 1.
DR PROSITE; PS00805; CALRETICULIN_REPEAT; 2.
DR Endoplasmic reticulum; Calcium-binding; Repeat; Signal; Glycoprotein.
DR SIGNAL 1 25 POTENTIAL.
DR CHAIN 26 416 CALRETICULIN.
DR CARBOHYD 57 57 N-LINKED (GLCNAC. .) (POTENTIAL).
DR CARBOHYD 157 157 N-LINKED (GLCNAC. .) (POTENTIAL).
DR SITE 413 416 PREVENT SECRETION FROM ER (POTENTIAL).
DR SEQUENCE 416 AA; 48136 MW; 565FEC3489F77CA7 CRC64;

Query Match 60.9%; Score 207; DB 1; Length 416;
Best Local Similarity 64.3%; Pred No. 5, 9e-18;
Matches 36; Conservative 7; Mismatches 13; Indels 0; Gaps 0;

QY 5 GDSYNNIMFGPDICGPGTKKVVHFNKGNVNLINKDIRCKDDETHLYTLIVRPD 60
Db 130 GDTPSIMFGPDICGPGTKKVVHFNKGNVNLINKDIRCKDDETHLYTLIVRPD 185

RESULT 13
CRTC_PRUAR STANDARD; PRT; 421 AA.
ID CRTC_PRUAR
AC Q9XF98;
DT 20-AUG-2001 (Rel. 40, Created)
DT 20-AUG-2001 (Rel. 40, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE CALRETICULIN PRECURSOR.
OS Prunus armeniaca (Apricot).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids I; Rosales; Rosaceae; Prunus.
OX NCBI_TaxID=36596;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97435975; PubMed=9290642;
RA Coughlan S.J., Hastings C., Winfrey R. Jr.;
RT "Cloning and characterization of the calreticulin gene from Ricinus
RT communis L.";
RL Plant Mol. Biol. 34:897-911(1997).
CC -!- FUNCTION: THIS PROTEIN BINDS CALCIUM. THERE ARE BOTH HIGH AND
CC LOW AFFINITY CALCIUM-BINDING SITES.
CC -!- SUBCELLULAR LOCATION: ENDOPLASMIC RETICULUM LUMEN.
CC -!- SIMILARITY: BELONGS TO THE CALRETICULIN FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; U74631; AAB71420.1; -
DR EMBL; U74630; AAB71419.1; -
DR Mendel; 10452; Ricco:1166; 10452.
DR InterPro; IPR001580; Calreticulin.
DR Pfam; PF00262; calreticulin; 1.
DR PRINTS; PR00626; CALRETICULIN.
DR ProDom; PD001866; Calreticulin; 1.
DR PROSITE; PS00014; ER_TARGET; 1.
DR PROSITE; PS00803; CALRETICULIN_1; 1.
DR PROSITE; PS00804; CALRETICULIN_2; 1.
DR PROSITE; PS00805; CALRETICULIN_REPEAT; 2.
DR Endoplasmic reticulum; Calcium-binding; Repeat; Signal; Glycoprotein.
DR SIGNAL 1 22 POTENTIAL.
DR CHAIN 23 421 CALRETICULIN.
DR CARBOHYD 56 56 N-LINKED (GLCNAC. .) (POTENTIAL).
DR CARBOHYD 156 156 N-LINKED (GLCNAC. .) (POTENTIAL).
DR SITE 418 421 PREVENT SECRETION FROM ER (POTENTIAL).
DR SEQUENCE 421 AA; 48416 MW; 4F3F94CBAA6C6690 CRC64;
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CC -----
DR EMBL; AF134733; AAD32207.1; -
DR InterPro; IPR001580; Calreticulin.
DR InterPro; IPR000886; ER.target.
DR Pfam; PF00262; calreticulin; 1.
DR PRINTS; PR00626; CALRETICULIN.
DR ProDom; PD001866; Calreticulin; 1.
DR PROSITE; PS00014; ER_TARGET; 1.
DR PROSITE; PS00803; CALRETICULIN_1; 1.
DR PROSITE; PS00804; CALRETICULIN_2; 1.
DR PROSITE; PS00805; CALRETICULIN_REPEAT; 2.
DR Endoplasmic reticulum; Calcium-binding; Repeat; Signal; Glycoprotein.
DR SIGNAL 1 22 POTENTIAL.
DR CHAIN 23 421 CALRETICULIN.
DR CARBOHYD 56 56 N-LINKED (GLCNAC. .) (POTENTIAL).
DR CARBOHYD 156 156 N-LINKED (GLCNAC. .) (POTENTIAL).
DR SITE 418 421 PREVENT SECRETION FROM ER (POTENTIAL).
DR SEQUENCE 421 AA; 48416 MW; 4F3F94CBAA6C6690 CRC64;

Query Match 60.0%; Score 204; DB 1; Length 421;
Best Local Similarity 62.5%; Pred No. 1, 4e-17;
Matches 35; Conservative 7; Mismatches 14; Indels 0; Gaps 0;

QY 5 GDSYNNIMFGPDICGPGTKKVVHFNKGNVNLINKDIRCKDDETHLYTLIVRPD 60
Db 129 GDTPSIMFGPDICGPGTKKVVHFNKGNVNLINKDIRCKDDETHLYTLIVRPD 184

RESULT 14
CRTC_RICCO STANDARD; PRT; 415 AA.
ID CRTC_RICCO
AC P93508;
DT 20-AUG-2001 (Rel. 40, Created)
DT 20-AUG-2001 (Rel. 40, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE CALRETICULIN PRECURSOR.
OS Ricinus communis (Castor bean).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids I; Malpighiales; Euphorbiaceae; Ricinus.
OX NCBI_TaxID=3988;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97435975; PubMed=9290642;
RA Coughlan S.J., Hastings C., Winfrey R. Jr.;
RT "Cloning and characterization of the calreticulin gene from Ricinus
RT communis L.";
RL Plant Mol. Biol. 34:897-911(1997).
CC -!- FUNCTION: THIS PROTEIN BINDS CALCIUM. THERE ARE BOTH HIGH AND
CC LOW AFFINITY CALCIUM-BINDING SITES.
CC -!- SUBCELLULAR LOCATION: ENDOPLASMIC RETICULUM LUMEN.
CC -!- SIMILARITY: BELONGS TO THE CALRETICULIN FAMILY.
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; U74631; AAB71420.1; -
DR EMBL; U74630; AAB71419.1; -
DR Mendel; 10452; Ricco:1166; 10452.
DR InterPro; IPR001580; Calreticulin.
DR Pfam; PF00262; calreticulin; 1.
DR PRINTS; PR00626; CALRETICULIN.
DR ProDom; PD001866; Calreticulin; 1.
DR PROSITE; PS00014; ER_TARGET; 1.
DR PROSITE; PS00803; CALRETICULIN_1; 1.
DR PROSITE; PS00804; CALRETICULIN_2; 1.
DR PROSITE; PS00805; CALRETICULIN_REPEAT; 2.
DR Endoplasmic reticulum; Calcium-binding; Repeat; Signal; Glycoprotein.
DR SIGNAL 1 22 POTENTIAL.
DR CHAIN 23 421 CALRETICULIN.
DR CARBOHYD 56 56 N-LINKED (GLCNAC. .) (POTENTIAL).
DR CARBOHYD 156 156 N-LINKED (GLCNAC. .) (POTENTIAL).
DR SITE 418 421 PREVENT SECRETION FROM ER (POTENTIAL).
DR SEQUENCE 421 AA; 48416 MW; 4F3F94CBAA6C6690 CRC64;
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DR PROSITE; PS00803; CALRETICULIN\_1; 1.  
DR PROSITE; PS00804; CALRETICULIN\_2; 1.  
DR PROSITE; PS00805; CALRETICULIN\_REPEAT; 2.  
KW Endoplasmic reticulum; Calcium-binding; Repeat; Signal; Glycoprotein.  
FT SIGNAL 1 20 POTENTIAL.  
FT CHAIN 21 415  
FT CARBOHYD 52 52 N-LINKED (GLCNAC. .) (POTENTIAL).  
FT CARBOHYD 152 152 N-LINKED (GLCNAC. .) (POTENTIAL).  
FT SITE 412 415 PREVENT SECRETION FROM ER (POTENTIAL).  
SQ SEQUENCE 415 AA; 47522 MW; DD3F452E76CC7F8C CRC64;

Query Match 59.4%; Score 202; DB 1; Length 415;  
Best Local Similarity 60.7%; Pred. No. 2.4e-17;  
Matches 34; Conservative 9; Mismatches 13; Indels 0; Gaps 0;

QY 5 GDSEYNIMFGPDICGPTKKVHIFNYKGNVINKDIRCKDDEFTHLYTLVLRPD 60  
||: ||:||||| ||||| || ||||| ||: ||: ||: ||:|||||  
Db 125 GDTPTYSIMFGPDICGYSTKKVHAILNYNDTNHLIKKEVPCETDQLTHVYTLVLRPD 180

## RESULT 15

CR2\_ARATH  
ID CR2\_ARATH STANDARD; PRT; 424 AA.  
AC Q38858; O80486; O04152;  
DT 20-AUG-2001 (Rel. 40, Created)  
DT 20-AUG-2001 (Rel. 40, Last sequence update)  
DE CALRETICULIN 2 PRECURSOR.  
GN CR2 OR CRPL OR T12M4.8.  
OS Arabidopsis thaliana (Mouse-ear cress).  
OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
OC eurosids II; Brassicales; Brassicaceae; Arabidopsi.  
OX NCBI\_TaxID:3702;  
RN [1]  
RP SKOURNCE FROM N.A.  
RC STRAIN-CV. COLUMBIA;  
RA Vynolaka V.S., Schwartz J.R., Toriumi M., Yu G., Oji O., Kwan A.,  
Liu S., Li J., Arasujo R., Au M., Brendel V., Buehler E., Conway A.B.,  
Conway A.R., Dewar K., Feng K., Kim C., Kurtz D., Li Y., Palm C.J.,  
Shinn P., Sun H., Davis R.W., Ecker J.R., Federspiel N.A.,  
Theologis A.;  
RL Submitted (NOV-1997) to the EMBL/GenBank/DBJ databases.  
RN [2]  
RP SEQUENCE OF 1-174 FROM N.A.  
RX MEDLINE-97303616; PubMed-9159940;  
RA Nelson D.E., Glaunsinger B., Bohnert H.J.;  
RT "Abundant accumulation of the calcium-binding molecular chaperone  
calreticulin in specific floral tissues of Arabidopsis thaliana.";  
RL Plant Physiol. 114:29-37(1997).  
RN [3]  
RP SEQUENCE OF 16-424 FROM N.A.  
RC STRAIN-CV. LANDSBERG ERCTA; TISSUE=flower;  
RA Benedetti C.E., Turner J.G.;  
RT "Nucleotide sequence of an Arabidopsis thaliana cDNA encoding a  
protein homologous to plant and animal calreticulins.";  
RL (in) Plant Gene Register PGR95-047.  
CC [-] FUNCTION: THIS PROTEIN BINDS CALCIUM. THERE ARE BOTH HIGH AND  
LOW AFFINITY CALCIUM-BINDING SITES (BY SIMILARITY).  
CC [-] SUBCELLULAR LOCATION: ENDOPLASMIC RETICULUM LUMEN (BY SIMILARITY).  
CC [-] SIMILARITY: BELONGS TO THE CALRETICULIN FAMILY.  
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CC -----  
DR EMBL; AAC003114; AAC24083.1; ALT\_SEQ.  
DR EMBL; U66344; AAC49696.1; ALT\_INIT.

DR EMBL; U27698; AAA80652.1; -.  
DR HSP; P00368; ARXN  
DR SWISS-2DPAGE; Q38858; ARATH.  
DR Mendel; 6599; Arath;1166;6599.  
DR Mendel; 31147; Arath;1166;31147.  
DR Mendel; 16506; Arath;1166;16506.  
DR InterPro; IPR001580; Calreticulin.  
DR InterPro; IPR000886; ER\_target.  
DR Pfam; PF00262; calreticulin; 1.  
DR PRINTS; P00626; CALRETICULIN.  
DR ProDom; PD001866; Calreticulin; 1.  
DR PROSITE; PS00014; ER\_TARGET; 1.  
DR PROSITE; PS00803; CALRETICULIN\_1; 1.  
DR PROSITE; PS00804; CALRETICULIN\_2; 1.  
DR PROSITE; PS00805; CALRETICULIN\_REPEAT; 2.  
KW Endoplasmic reticulum; Calcium-binding; Repeat; Signal; Glycoprotein;  
KW Multigene family.  
FT SIGNAL 1 22 POTENTIAL.  
FT CHAIN 23 424 CALRETICULIN 2.  
FT CARBOHYD 59 59 N-LINKED (GLCNAC. .) (POTENTIAL).  
FT SITE 421 424 PREVENT SECRETION FROM ER (POTENTIAL).  
FT CONFLICT 16 19 LVAI -> NSAR (IN REF. 3).  
FT CONFLICT 155 155 G -> E (IN REF. 1).  
FT CONFLICT 236 236 P -> T (IN REF. 3).  
FT CONFLICT 408 408 V -> E (IN REF. 3).  
SQ SEQUENCE 424 AA; 48084 MW; 514385BAE810DD7 CRC64;

Query Match 59.4%; Score 202; DB 1; Length 424;  
Best Local Similarity 62.5%; Pred. No. 2.5e-17;  
Matches 35; Conservative 7; Mismatches 14; Indels 0; Gaps 0;

QY 5 GDSEYNIMFGPDICGPTKKVHIFNYKGNVINKDIRCKDDEFTHLYTLVLRPD 60  
||: ||:||||| ||||| || ||||| ||: ||: ||: ||:|||||  
Db 127 GDTPTYSIMFGPDICGYSTKKVHAILTYNGANHLIKKDVPCETDQLTHVYTLVLRPD 182

Search completed: January 9, 2002, 15:12:15  
Job time: 657 sec

Query Match 90.9%; Score 309; DB 5; Length 421;  
Best Local Similarity 91.1%; Pred. No. 1.7e-29;  
Matches 55; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

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RESULT 2
Q26268 AC Q26268 PRELIMINARY; PRT; 405 AA.
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE CALRETICULIN
OS Aplysia californica (California sea hare).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Opisthobranchia; Anaspidea;
OC Aplousididae; Aplysia.
OX NCBI_TaxID:6500;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-93098937; PubMed 1463604;
RA Kennedy T.E., Kuhl D., Barrilal A., Sweatt J.D., Kandel E.R.;
RT "Long-term sensitization training in Aplysia leads to an increase in
calreticulin, a major presynaptic calcium-binding protein.";
RL Neuron 9:1013-1024(1992).
DR EMBL: S51239; AAB24569.1; -
DR InterPro: IPR000886; ER.target.
DR InterPro: IPR001580; Calreticulin.
DR Pfam: PF00262; calreticulin; 1.
DR PRINTS: PR00626; Calreticulin.
DR ProDom: PD001866; Calreticulin; 1.
DR PROSITE: PS00803; CALRETICULIN_1; 1.
DR PROSITE: PS00804; CALRETICULIN_2; 1.
DR PROSITE: PS00805; CALRETICULIN_REPEAT; 3.
DR PROSITE: PS00014; ER_TARGET; UNKNOWN_1.
SQ SEQUENCE 405 AA; 46738 MW; 14CAA201840D1D69 CRC64;

Query Match 89.7%; Score 305; DB 5; Length 405;
Best Local Similarity 86.9%; Pred. No. 5e-29;
Matches 53; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY 1 TMHGDSEYNIMFGPDICGPGTKKVVHVIYFKGNVLINKDIRCKDDETHLYTLIVRPD 60
Db 116 SDMHGSEYNIMFGPDICGPGTKKVVHVIYFKGNVLINKDIRCKDDETHLYTLIVRPD 175

QY 61 N 61
Db 176 N 176

RESULT 3
Q9PTX7 ID Q9PTX7 PRELIMINARY; PRT; 318 AA.
AC Q9PTX7
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE CALRETICULIN (FRAGMENT).
OS Lampetia roissneri.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Hyperoartia;
OC Petromyzontiformes; Petromyzontidae; Lampetra.
OX NCBI_TaxID:7753;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-20063780; PubMed-10594174;
RA Kuraku S., Hoshiyama D., Katoh K., Suga H., Miyata T.;
RT "Monophyly of lampreys and hagfishes supported by nuclear DNA-coded
genes.";
RL J. Mol. Evol. 49:729-735(1999).
DR EMBL: AB025328; BAA88481.1; -
DR InterPro: IPR000886; ER.target.
DR InterPro: IPR001580; Calreticulin.
DR Pfam: PF00262; Calreticulin; 1.
DR PRINTS: PR00626; Calreticulin.
DR ProDom: PD001866; Calreticulin; 1.
DR PROSITE: PS00804; CALRETICULIN_2; 1.

Query Match 87.1%; Score 296; DB 13; Length 343;
Best Local Similarity 86.9%; Pred. No. 5.2e-28;
Matches 53; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 1 TMHGDSEYNIMFGPDICGPGTKKVVHVIYFKGNVLINKDIRCKDDETHLYTLIVRPD 60
Db 92 TEMHGESEYNIMFGPDICGPGTKKVVHVIYFKGNVLINKDIRCKDDETHLYTLIVRPD 151

QY 61 N 61
Db 152 N 152

RESULT 5
Q9U916 ID Q9U916 PRELIMINARY; PRT; 406 AA.
AC Q9U916;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE CALRETICULIN
OS Drosophila melanogaster (Fruit fly).
OS Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;

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RESULT	6
ID Q91710	PRELIMINARY; PRT; 411 AA.
AC Q91710;	
DT 01-JAN-1998	(TREMBLrel. 05, Created)
DT 01-JAN-1998	(TREMBLrel. 05, Last sequence update)
DT 01-JUN-2001	(TREMBLrel. 17, Last annotation update)
DE CALRETICULIN PRECURSOR (FRAGMENT).	
OS Xenopus laevis	(African clawed frog).
OC Eukaryota;	Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia;	Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
OC Xenopodinae;	Xenopus.
OX NCBI_TaxID=8355;	
[1]	
RN SEQUENCE FROM N.A.	
KC TISSUE=BRAIN;	
RX MEDLINE=93074997; PubMed=1445218;	
RC Treves S., Zorzato F., Pozzan T.;	
RT "Identification of calreticulin isoforms in the central nervous system.";	
RL Biochem. J. 287:579-581(1992).	
DR EMBL; X67597; CAA47866.1; -.	
DR InterPro; IPR000886; ER_target.	
DR InterPro; IPR001580; Calreticulin.	
DR Pfam; PF00262; calreticulin.1.	
DR PRINTS; PR00626; CALRETICULIN.	
DR ProDom; PD001866; Calreticulin.1.	
DR PROSITE; PS00803; CALRETICULIN_1; 1.	
DR PROSITE; PS00804; CALRETICULIN_2; 1.	
DR PROSITE; PS00805; CALRETICULIN_REPEAT; 2.	
DR PROSITE; PS00014; ER_TARGET; UNKNOWN_1.	
KW Signal.	
FT NON_TER	1 12
FT SIGNAL	<1 12 POTENTIAL.
FT CHAIN	13 411 CALRETICULIN.
SQ SEQUENCE	411 AA; 48344 MW; 891DA6GE00EBBEFA CRC64;

Qy	1	TDHGDSEYNIMEGPDICGGPTKKVHVIFNYKGNVLINIKDKIRCKODEFTHLTYTLIVRPD	60
Dd	121	TDHMGESEYNIMEGPDICGGPTKKVHVIFNYKGNLIQINKDIRSKADVVSHLYTLIVRPD	180
Qy	61	N 61 	
Dd	181	N 181	
RESULT	8		
Q16893			
ID	Q16893	PRELIMINARY; PRT;	410 AA.
AC	Q16893;		
DT	01-NOV-1996	(TREMBlrel. 01, Created)	
DT	01-JAN-1999	(TREMBlrel. 09, Last sequence update)	
DT	01-JUN-2001	(TREMBlrel. 17, Last annotation update)	
DE	CALRETICULIN.		

GN CRT-1.  
OS Amblyomma americanum.  
OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Acari;  
OC Parasitiformes; Ixodida; Ixodidae; Amblyomma.  
OX NCBI\_TaxID:6943;  
RN [1]  
RP SEQUENCE OF 49-410 FROM N.A.  
RC TISSUE SALIVARY GLANDS;  
RA Jaworski D.C., Simmen F.A., Lamoreaux W.J., Coons L.B., Muller M.T.,  
RA Newdham G.R.;  
RT "A secreted calreticulin protein in Ixodid tick (Amblyomma americanum)  
KT saliva";  
RL J. Insect Physiol. 41:369-375(1995).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC TISSUE SALIVARY GLANDS;  
RA Juorinki D.C.;  
RL Submitted (MAR-1994) to the EMBL/GenBank/DBJ databases.  
RN [3]  
RP SEQUENCE FROM N.A.  
RC TISSUE SALIVARY GLANDS;  
RA Fain-Thornton J.M., Jaworski D.C., Needham G.R.;  
RL Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.  
DR EMBL; U07708; AAC79094.1; -.  
DR Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;  
DR InterPro; IPR000886; ER\_target.  
DR InterPro; IPR001580; Calreticulin.  
DR Pfam; PF00262; calreticulin; 1.  
DR PRINTS; PR00626; CALRETICULIN.  
DR ProDom; PD001866; Calreticulin; 1.  
DR PROSITE; PS00803; CALRETICULIN\_1; 1.  
DR PROSITE; PS00805; CALRETICULIN\_REPEAT; 3.  
DR PROSITE; PS00014; ER\_TARGET; UNKNOWN\_1.  
DR SEQUENCE 410 AA; 47485 MW; 32CCB8750A17DC54 CRC64;  
  
Query Match 82.6%; Score 281; DB 5; Length 410;  
Best Local Similarity 84.7%; Pred. No. 4.2e-26;  
Matches 50; Conservative 4; Mismatches 5; Indels 0; Gaps 0;  
  
QY 3 MHGDSYNIHFGPDICGPGTKKVVHIFNYKGNVLINKDIRCKDDFTHTLYLVKPDN 61  
DB 121 LHGESPKIMFPPDICGPGTKKVVHIFNYKGNVLINKDIRCKDDFTHTLYLVKPDN 179  
  
RESULT 9  
Q97372 PRELIMINARY; PRT; 387 AA.  
AC Q97372;  
DT 01-MAY-1999 (TREMBlrel. 10, Created)  
DT 01-MAY-1999 (TREMBlrel. 10, Last sequence update)  
DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)  
DE CALRETICULIN PRECURSOR.  
OS Dirofilaria immitis.  
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Spirurida; Filarioidea;  
OC Onchocercidae; Dirofilaria.  
OX NCBI\_TaxID:6287;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE 99094497; PubMed:9879888;  
RA Tsuji N., Morales T.H., Ozols V.V., Carmody A.B., Chandrashekar R.;  
RT "Molecular characterization of a calcium-binding protein from the  
RT filarial parasite Dirofilaria immitis";  
RL Mol. Biochem. Parasitol. 97:69-79(1998).  
DR EMBL; AF052978; AAD03405.1; -.  
DR InterPro; IPR001580; Calreticulin.  
DR Pfam; PF00262; calreticulin; 1.  
DR PRINTS; PR00626; CALRETICULIN.  
DR ProDom; PD001866; Calreticulin; 1.  
DR PROSITE; PS00803; CALRETICULIN\_1; 1.  
DR PROSITE; PS00804; CALRETICULIN\_2; 1.  
DR PROSITE; PS00805; CALRETICULIN\_REPEAT; 3.  
KW Signal.  
FT SIGNAL 1 18 POTENTIAL.

FT CHAIN 19 387 CALRETICULIN.  
SQ SEQUENCE 387 AA; 44941 MW; E7741BF6AAFA5885 CRC64;  
  
Query Match 80.6%; Score 274; DB 5; Length 387;  
Best Local Similarity 80.0%; Pred. No. 2.8e-25;  
Matches 48; Conservative 5; Mismatches 7; Indels 0; Gaps 0;  
  
QY 2 DMHGSEYNIHFGPDICGPGTKKVVHIFNYKGNVLINKDIRCKDDFTHTLYLVKPDN 61  
DB 119 DFHGETPYNIHFGPDICGPGTKKVVHIFNYKGNVLINKDIRCKDDFTHTLYLVKPDN 178  
  
RESULT 10  
Q9PUC1 PRELIMINARY; PRT; 417 AA.  
ID Q9PUC1;  
AC Q9PUC1;  
DT 01-MAY-2000 (TREMBlrel. 13, Created)  
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)  
DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)  
DE CALRETICULIN.  
OS Brachydanio rerio (Zebrafish) (Zebra danio).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;  
OC Cypriniformes; Cyprinidae; Rasbora; Danio.  
OX NCBI\_TaxID:7955;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Rubinstein A.L., Lee D., Luo R., Henion P.D., Halpern M.E.;  
RT "Genes Dependent on zebrafish cyclops Function Identified by AFLP  
RT Differential Gene Expression Screen";  
RL Genesis 0:0-0(1999).  
DR EMBL; AF195882; AAF13700.1; -.  
DR InterPro; IPR000886; ER\_target.  
DR InterPro; IPR001580; Calreticulin.  
DR Pfam; PF00262; calreticulin; 1.  
DR PRINTS; PR00626; CALRETICULIN.  
DR ProDom; PD001866; Calreticulin; 1.  
DR PROSITE; PS00803; CALRETICULIN\_1; 1.  
DR PROSITE; PS00804; CALRETICULIN\_2; 1.  
DR PROSITE; PS00805; CALRETICULIN\_REPEAT; 3.  
DR PROSITE; PS00014; ER\_TARGET; UNKNOWN\_1.  
DR SEQUENCE 417 AA; 48723 MW; 2000C5B4004699B6 CRC64;  
  
Query Match 79.4%; Score 270; DB 13; Length 417;  
Best Local Similarity 80.0%; Pred. No. 9.2e-25;  
Matches 48; Conservative 6; Mismatches 6; Indels 0; Gaps 0;  
  
QY 1 TOMHGDSEYNIHFGPDICGPGTKKVVHIFNYKGNVLINKDIRCKDDFTHTLYLVKPDN 60  
DB 120 TEMHGESYIIMFGPDICGPGTKKVVHIFNYKGNVLINKDIRCKDDFTHTLYLVKPDN 179  
  
RESULT 11  
O18478 PRELIMINARY; PRT; 375 AA.  
ID O18478;  
AC O18478;  
DT 01-JAN-1998 (TREMBlrel. 05, Created)  
DT 01-JAN-1998 (TREMBlrel. 05, Last sequence update)  
DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)  
DE RAL-1 PROTEIN (FRAGMENT).  
OS Litomosoides sigmodontis.  
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Spirurida; Filarioidea;  
OC Onchocercidae; Litomosoides.  
OX NCBI\_TaxID:42156;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA MacLennan K., Hoffman W.H., Taylor D.W.;  
RL Submitted (SEP-1997) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AJ001621; CAA04877.1; -.  
DR InterPro; IPR001580; Calreticulin.  
DR Pfam; PF00262; calreticulin; 1.



```

DR PRINTS: PR00626; CALRETICULIN.
DR PRODom; PD001866; CALRETICULIN_1.
DR PROSITE; PS00803; CALRETICULIN_1; 1.
DR PROSITE; PS00804; CALRETICULIN_2; 1.
DR PROSITE; PS00805; CALRETICULIN_REPEAT; 3.
FT NON_TER 375
SQ SEQUENCE 375 AA; 43842 MW; 03F7642FBFF7A5B8 CRC64;

Query Match 79.1%; Score 269; DB 5; Length 375;
Best Local Similarity 78.3%; Pred. No. 1.le-24;
Matches 47; Conservative 6; Mismatches 7; Indels 0; Gaps 0;

Qy 2 DMHGSEYNIMFGPDICGPGTKVHVIFNYKGNVLINKDIRCKDDETHLYTLIVRPDN 61
Db 119 DFHGETPYHIMFGPDICGPGTKVHVIFNYKGNVHMIIKKDIRCKDDVETHLYTLIVNSDN 178

RESULT 12
O76961 PRELIMINARY; PRT; 403 AA.
ID O76961; AC O76961;
DT 01-NOV-1998 (TReMBLrel. 08, Created)
DT 01-NOV-1998 (TReMBLrel. 08, Last sequence update)
DT 01-JUN-2001 (TReMBLrel. 17, Last annotation update)
DE CALRETICULIN PRECURSOR.
GN CRT.
OS Necator americanus.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Strongylida;
OC Ancylostomatidae; Ancylostomatidae; Bunostominae; Necator.
OX NCBI_TaxID=51031;
RN [1]
RP SEQUENCE FROM N.A.
RA Pritchard D.I., Brown A., McElroy P., Loukas A., Girdwood K.,
RA Berry C., Fullkrug R., Beck E.;
RT "Calreticulin is a hookworm allergen.";
RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ006790; CAA07234.1; -.
DR InterPro; IPR000886; ER_target.
DR InterPro; IPR001580; Calreticulin.
DR Pfam; PF00262; calreticulin; 1.
DR PRINTS; PR00626; CALRETICULIN.
DR PRODom; PD001866; Calreticulin; 1.
DR PROSITE; PS00803; CALRETICULIN_1; 1.
DR PROSITE; PS00804; CALRETICULIN_2; 1.
DR PROSITE; PS00805; CALRETICULIN_REPEAT; 3.
DR PROSITE; PS00014; ER_TARGET; UNKNOWN_1.
KW Signal; Allergen.
FT SIGNAL 1
FT SIGNAL 16 POTENTIAL.
SQ SEQUENCE 403 AA; 46833 MW; 21F3850515487B6F CRC64;

Query Match 76.9%; Score 261.5; DB 5; Length 403;
Best Local Similarity 77.0%; Pred. No. 9.5e-24;
Matches 47; Conservative 6; Mismatches 7; Indels 1; Gaps 1;

Qy 1 TDMHGSEYNIMFGPDICGPGTKVHVIFNYKGNVLINKDIRCKDDETHLYTLIVRPD 60
Db 117 SDFHGETPYHIMFGPDICGPGTKVHVIFNYKGNVHMIIKKDIRCKDDVETHLYTLIVNSDN 175

Qy 61 N 61
Db 176 N 176

RESULT 13
Q26514 PRELIMINARY; PRT; 350 AA.
ID Q26514; AC Q26514;
DT 01-NOV-1996 (TReMBLrel. 01, Created)
DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)
DT 01-JUN-2001 (TReMBLrel. 17, Last annotation update)
DE CALRETICULIN (FRAGMENT).

```

```

GN RAL-1.
OS Schistosoma japonicum (Blood fluke).
OC Eukaryota; Metazoa; Platyhelminthes; Rhabditophora; Neodermata;
OC Trematoda; Digenea; Strigeidida; Schistosomatidae; Schistosomatidae;
OC Schistosoma.
OX NCBI_TaxID=6182;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CHINESE;
RA Huggins M.C., Moloney N.A.;
RL Submitted (AUG-1993) to the EMBL/GenBank/DBJ databases.
DR EMBL; M80524; AAA29917.1; -.
DR InterPro; IPR000886; ER_target.
DR InterPro; IPR001580; Calreticulin.
DR Pfam; PF00262; calreticulin; 1.
DR PRINTS; PR00626; CALRETICULIN.
DR PRODom; PD001866; Calreticulin; 1.
DR PROSITE; PS00803; CALRETICULIN_1; 1.
DR PROSITE; PS00804; CALRETICULIN_2; 1.
DR PROSITE; PS00805; CALRETICULIN_REPEAT; 1.
DR PROSITE; PS00014; ER_TARGET; UNKNOWN_1.
FT NON_TER 1
SQ SEQUENCE 350 AA; 40385 MW; 30FAB4E8BB685D1C CRC64;

Query Match 73.5%; Score 250; DB 5; Length 350;
Best Local Similarity 75.9%; Pred. No. 2e-22;
Matches 44; Conservative 6; Mismatches 8; Indels 0; Gaps 0;

Qy 4 HCDSEYNIMFGPDICGPGTKVHVIFNYKGNVLINKDIRCKDDETHLYTLIVRPDN 61
Db 76 HGETPYKIMFGPDICGPGTKVHVIFNYKGNVHMIIKKDIRCKDDQKTHLYTLIVRPDN 133

RESULT 14
O45034 PRELIMINARY; PRT; 396 AA.
ID O45034; AC O45034;
DT 01-JUN-1998 (TReMBLrel. 06, Created)
DT 01-JUN-1998 (TReMBLrel. 06, Last sequence update)
DT 01-JUN-2001 (TReMBLrel. 17, Last annotation update)
DE CALRETICULIN.
OS Schistosoma japonicum (Blood fluke).
OC Eukaryota; Metazoa; Platyhelminthes; Rhabditophora; Neodermata;
OC Trematoda; Digenea; Strigeidida; Schistosomatidae; Schistosomatidae;
OC Schistosoma.
OX NCBI_TaxID=6182;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=PHILIPPINE (MINDORO);
RA Scott J.C.;
RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF044408; AAC00515.1; -.
DR InterPro; IPR000886; ER_target.
DR InterPro; IPR001580; Calreticulin.
DR Pfam; PF00262; calreticulin; 1.
DR PRINTS; PR00626; CALRETICULIN.
DR PRODom; PD001866; Calreticulin; 1.
DR PROSITE; PS00803; CALRETICULIN_1; 1.
DR PROSITE; PS00804; CALRETICULIN_2; 1.
DR PROSITE; PS00805; CALRETICULIN_REPEAT; 2.
DR PROSITE; PS00014; ER_TARGET; UNKNOWN_1.
SQ SEQUENCE 396 AA; 45813 MW; C57394C6FB4CD77B CRC64;

Query Match 73.5%; Score 250; DB 5; Length 396;
Best Local Similarity 75.9%; Pred. No. 2.3e-22;
Matches 44; Conservative 6; Mismatches 8; Indels 0; Gaps 0;

Qy 4 HCDSEYNIMFGPDICGPGTKVHVIFNYKGNVLINKDIRCKDDETHLYTLIVRPDN 61
Db 122 HGETPYKIMFGPDICGPGTKVHVIFNYKGNVHMIIKKDIRCKDDQKTHLYTLIVRPDN 179

```

```
RESULT 15
Q9U5G0
ID Q9U5G0 PRELIMINARY; PRT; 321 AA.
AC Q9U5G0;
DT 01-MAY-2000 (TRENBLrel. 13, Created)
DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TRENBLrel. 17, Last annotation update)
DE CALRETICULIN (FRAGMENT).
OS Eptatretus burgeri (inshore hagfish).
OC Eukaryota; Metazoa; Chordata; Craniata; Hyperotreti; Myxiniiformes;
OC Myxiniidae; Eptatretinae; Eptatretus.
OX NCBI_TaxID:7764;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE: LIVER;
RX MEDLINE:20063780; Pubmed 10594174;
RA Kuraku S., Hoshiyama D., Katoh K., Suga H., Miyata T.;
RT "Monophyly of lampreys and hagfishes supported by nuclear DNA-coded
RT genes.";
RL J. Mol. Evol. 49:729-735(1999).
DR EMBL; AH025323; BAA88476.1; -.
DR InterPro; IPR000886; ER_target.
DR InterPro; IPR001580; Calreticulin.
DR Pfam; PF00262; calreticulin; 1.
DR PRINTS; PR00626; CALRETICULIN.
DR PRODOM; PD001866; Calreticulin; 1.
DR PROSITE; PS00804; CALRETICULIN_2; 1.
DR PROSITE; PS00805; CALRETICULIN_REPEAT; 3.
DR PROSITE; PS00014; ER_TARGET; UNKNOWN_1.
PT NON_TER 1
SQ SEQUENCE 321 AA; 37367 MW; 6E8DFA98D42F7AEF CRC64;
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Query Match 67.6%; Score 230; DB 13; Length 321;
Best Local Similarity 70.7%; Pred. No. 4.9e-20;
Matches 41; Conservative 8; Mismatches 9; Indels 0; Gaps 0;
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```
QY 3 MNGDSEYNIWPGDTCGPGTKKVVHVFNYKGNVLINKDIRCKDDFFTHLYTLIVRPD 60
DB 21 LAGESEYIWFPGDTCGPGTKKVVHVLNSKGNHLIKKEVKCKDDDMTHLYTLMLYPD 78
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Search completed: January 9, 2002, 15:03:28  
Job time: 270 sec

GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: January 9, 2002, 15:01:12 ; Search time 83.2 Seconds  
(without alignments)  
54.309 Million cell updates/sec

Title: US-09-828-000-4  
Perfect score: 340  
Sequence: 1 TDMHGEYINMGPDICGP.....IRKDDFTHLYTLIVRPDN 61

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 522463 seqs, 74073290 residues

Total number of hits satisfying chosen parameters: 522463

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A\_Geneseq\_1101.\*

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22: /SID88/gcgdata/geneseq/geneseqp/AA2001.DAT.*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	340	100.0	180	21	Human vasostatin (
2	340	100.0	400	21	Recombinant human
3	340	100.0	417	10	60 KD Ro (Ro/SSA)
4	340	100.0	417	20	Calreticulin. Hom
5	340	100.0	417	21	Human MBP-calretic
6	335	98.5	401	18	Calreticulin. Hom
7	290	85.3	403	17	Flea calreticulin
8	261	76.8	336	12	Partial sequence o
9	244	71.8	61	21	Recombinant human
10	235	69.1	60	21	Recombinant human
11	235	69.1	280	21	Recombinant delta-

12	202	59.4	415	22	AAB66341	Castor bean calret
13	202	59.4	415	22	AAB66343	Castor bean calret
14	194	57.1	312	21	AAG24609	Arabidopsis thalia
15	194	57.1	312	21	AAG47933	Arabidopsis thalia
16	194	57.1	332	21	AAG30998	Arabidopsis thalia
17	194	57.1	421	21	AAG24608	Arabidopsis thalia
18	194	57.1	421	21	AAG47932	Arabidopsis thalia
19	194	57.1	424	21	AAG24607	Arabidopsis thalia
20	194	57.1	424	21	AAG47931	Arabidopsis thalia
21	194	57.1	441	21	AAG30997	Arabidopsis thalia
22	194	57.1	444	21	AAG30996	Arabidopsis thalia
23	187	55.0	385	21	AAB32385	Human secreted pro
24	175	51.5	49	21	AA192353	Recombinant human
25	125.5	36.9	542	22	AAB66342	Castor bean calnex
26	120.5	35.4	593	16	AA171094	Calnexin sequence.
27	115.5	34.0	530	21	AAG26284	Arabidopsis thalia
28	115.5	34.0	530	21	AAG46611	Arabidopsis thalia
29	115.5	34.0	567	21	AAG46610	Arabidopsis thalia
30	107	31.5	122	20	AA100924	Human cClqR bindin
31	107	31.5	122	20	AA100926	Rat cClqR binding
32	106	31.2	417	21	AA177953	A. thaliana enviro
33	105.5	31.0	532	21	AAG04448	Arabidopsis thalia
34	105.5	31.0	548	21	AAG04447	Arabidopsis thalia
35	99	29.1	122	20	AA100925	Mouse cClqR bindin
36	98.5	29.0	394	21	AAG26285	Arabidopsis thalia
37	98.5	29.0	394	21	AAG46612	Arabidopsis thalia
38	84.5	24.9	394	21	AAG04449	Arabidopsis thalia
39	67.5	19.9	455	21	AAG17438	Arabidopsis thalia
40	67.5	19.9	455	21	AAG21851	Arabidopsis thalia
41	67.5	19.9	466	21	AAG17437	Arabidopsis thalia
42	67.5	19.9	466	21	AAG21850	Arabidopsis thalia
43	67.5	19.9	489	21	AAG17436	Arabidopsis thalia
44	67.5	19.9	497	21	AAG21849	Arabidopsis thalia
45	67.5	19.9	844	21	AAG45432	Arabidopsis thalia

#### ALIGNMENTS

RESULT 1  
 AA192351  
 ID AA192351 standard; Protein; 180 AA.  
 AC AA192351;  
 DT 10-AUG-2000 (first entry)  
 XX  
 DE Human vasostatin (calreticulin N-terminal 180 amino acids).  
 KW MBP-calreticulin; maltose binding protein; vasostatin; N-terminal;  
 KW angiogenesis; inhibition; endothelial cell; anti-angiogenic;  
 KW neuroprotective; antidiabetic; cytostatic; dermatological; hepatic;  
 KW immunosuppressive; antiinflammatory; anti-atherosclerotic;  
 KW gastrointestinal; anti-arthritis; ophthalmic.  
 XX Homo sapiens.  
 OS Synthetic.  
 XX  
 PN WO200020577-A1.  
 PD 13-APR-2000.  
 XX  
 PF 05-OCT-1999; 99WO-US23240.  
 XX  
 PR 06-OCT-1998; 98US-0103438.  
 XX  
 PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.  
 XX  
 PI Tosato G, Pike SE, Yao L;  
 XX  
 DR WPI; 2000-303767/26.  
 XX  
 PT Inhibiting endothelial cell growth and angiogenesis using calreticulin,

PT useful for suppressing tumor growth  
 XX Claim 4; Page 82; 99pp; English.  
 XX A novel method of inhibiting endothelial cell growth comprises  
 CC contacting the cells with calreticulin (or its fragments/variants).  
 CC Fragments of calreticulin causes at least 40% inhibition of angiogenesis,  
 CC tumor growth and/or endothelial cell growth (claimed). The method may be  
 CC used for inhibiting angiogenesis in a patient. The angiogenesis is  
 CC associated with a disease other than a tumor that is associated with  
 CC neovascularization (e.g. diabetic neuropathy, retrolental fibroplasia,  
 CC trachoma, neovascular glaucoma, psoriasis, angiofibromas, immune  
 CC inflammation, atherosclerosis, excessive wound repair, retinal  
 CC neovascularization, macular degeneration, corneal graft rejection,  
 CC contact lens overwear, Crohn's disease, non-immune inflammation,  
 CC rheumatoid arthritis, systemic lupus erythematosus, thyroiditis,  
 CC Goodpasture's syndrome, systemic vasculitis, scleroderma, Sjorgen's  
 CC syndrome, sarcoidosis and primary biliary cirrhosis). The method may  
 CC also be used for treating/inhibiting tumor growth especially  
 CC Kaposi's sarcoma (claimed).  
 XX Sequence 180 AA;  
 SQ

Query Match 100.0%; Score 340; DB 21; Length 180;  
 Best Local Similarity 100.0%; Pred. No. 4.3e-39;  
 Matches 61; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TDMHGEYNIMFGPDICGPGTKKHVIVNYKGNVLINKDIRCKDDETHLYTLIVRPD 60  
 |||||  
 DB 103 tdmhgdeynimfgpdicgpgtkkhvifnykgknlkirkckddefthlytlivrp 162

QY 61 N 61  
 DB 163 n 163

RESULT 2  
 AAY92350  
 ID AAY92350 standard; Protein; 400 AA.  
 XX  
 AC AAY92350;  
 XX  
 DT 10-AUG-2000 (first entry)  
 XX  
 DE Recombinant human MBP-calreticulin.  
 XX  
 KW MBP-calreticulin; maltose binding protein; angiogenesis; inhibition;  
 KW endothelial cell; anti-angiogenic; neuroprotective; antidiabetic;  
 KW cytostatic; dermatologic; immunosuppressive; antiinflammatory; hepatic;  
 KW anti-atherosclerotic; gastrointestinal; anti-arthritis; ophthalmic.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200020577-A1.  
 XX  
 PD 13-APR-2000.  
 XX  
 PF 05-OCT-1999; 99WO-US23240.  
 XX  
 PR 06-OCT-1998; 98US-0103438.  
 XX  
 PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.  
 XX  
 PI Tosato G, Pike SE, Yao L;  
 XX  
 DR WPI; 2000-303767/26.  
 XX  
 DR N-PSDB; AAA09346, AAA09347.  
 XX  
 XX Inhibiting endothelial cell growth and angiogenesis using calreticulin,  
 PT useful for suppressing tumor growth  
 XX Claim 4; Page 80-81; 99pp; English.

XX Recombinant human MBP-calreticulin comprises the sequence of human  
 CC calreticulin (see AAY92349) without the 17 N-terminal amino acids.  
 CC A novel method of inhibiting endothelial cell growth comprises  
 CC contacting the cells with calreticulin (or its fragments/variants).  
 CC Fragments of calreticulin causes at least 40% inhibition of  
 CC angiogenesis, tumor growth and/or endothelial cell growth (claimed). The  
 CC method may be used for inhibiting angiogenesis in a patient. The  
 CC angiogenesis is associated with a disease other than a tumor that is  
 CC associated with neovascularization (e.g. diabetic neuropathy, retrolental  
 CC fibroplasia, trachoma, neovascular glaucoma, psoriasis, angiofibromas,  
 CC immune inflammation, atherosclerosis, excessive wound repair, retinal  
 CC neovascularization, macular degeneration, corneal graft rejection,  
 CC contact lens overwear, Crohn's disease, non-immune inflammation,  
 CC rheumatoid arthritis, systemic lupus erythematosus, thyroiditis,  
 CC Goodpasture's syndrome, systemic vasculitis, scleroderma, Sjorgen's  
 CC syndrome, sarcoidosis and primary biliary cirrhosis). The method may  
 CC also be used for treating/inhibiting tumor growth especially  
 CC Kaposi's sarcoma (claimed).  
 XX Sequence 400 AA;  
 SQ

Query Match 100.0%; Score 340; DB 21; Length 400;  
 Best Local Similarity 100.0%; Pred. No. 1.2e-38;  
 Matches 61; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TDMHGEYNIMFGPDICGPGTKKHVIVNYKGNVLINKDIRCKDDETHLYTLIVRPD 60  
 |||||  
 DB 103 tdmhgdeynimfgpdicgpgtkkhvifnykgknlkirkckddefthlytlivrp 162

QY 61 N 61  
 DB 163 n 163

RESULT 3  
 AAP92276  
 ID AAP92276 standard; protein; 417 AA.  
 XX  
 AC AAP92276;  
 XX  
 DT 23-FEB-1990 (first entry)  
 XX  
 DE 60 kD Ro (Ro/SSA) antigen.  
 XX  
 KW Sjorens syndrome; systemic lupus erythematosus.  
 XX  
 OS Synthetic.  
 XX  
 PN WO8909273-A.  
 XX  
 PD 05-OCT-1989.  
 XX  
 PF 22-MAR-1989; 89WO-US01213.  
 XX  
 PR 22-MAR-1988; 88US-0171634.  
 XX  
 PA (TEXA ) UNIV OF TEXAS SYST.  
 XX  
 PI Sontheimer RD, Capra JD, McCauliffe DP;  
 XX  
 DR WPI; 1989-309537/42.  
 DR N-PSDB; AAP92276.  
 XX  
 XX DNA sequences encoding antigenic epitope(s) of Ro 60 kD autoantigen  
 PT - used in immunoassays to detect rheumatic disease  
 XX  
 PS Disclosure; Fig 2; 88pp; English.  
 XX  
 CC Synthetic peptides corresp. to an epitopic core of Ro antigen are  
 CC expressed recombinantly to detect autoantibodies, for identification  
 CC of autoimmune diseases. These epitopes are AAs 24-36, 23-36, 188-209,

CC or 241-255. The peptides may be substd. for ribonucleoprotein particle  
 CC antigens.

XX Sequence 417 AA;

Query Match 100.0%; Score 340; DB 10; Length 417;  
 Best Local Similarity 100.0%; Pred. No. 1.2e-38;  
 Matches 61; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TDMHGDSEYNIMFGPDICGPGTKKHVIFNKGKKNVLINKDIRCKDDETHLYTLIVRPD 60  
 |||||  
 Db 120 tdmhgdseynimfgpdicpgtkkhvifnykgknvlinkdirckddefthlytlivrp 179

QY 61 N 61

Db 180 n 180

RESULT 4

AA00927  
 ID AAY00927 standard; Protein; 417 AA.

XX  
 AC AAY00927;

XX 28-MAY-1999 (first entry)

XX Calreticulin.

XX Clq and collectin receptor; cClqR binding domain; complement ubiquitin;  
 KW CUB functionality; inhibitor; complement activation; inflammation;  
 KW myocardial infarction; brain ischaemia; gut ischaemia; amyloid plaque;  
 KW rheumatoid arthritis; systemic lupus erythematosus; Alzheimer's disease;  
 KW immune complex nephritis; therapy.

XX Homo sapiens.

XX WO9907406-A1.

XX 18-FEB-1999.

XX 12-AUG-1998; 98WO-GB02430.

XX 12-AUG-1997; 97GB-0016998.

XX (UYLE-) UNIV LEICESTER.

XX Schwaebler W;

XX WPI; 1999-180404/15.

XX Use of a cClqR binding domain - to modulate complement ubiquitin  
 (CUB) functionality.

XX Disclosure; Page 26-27; 31pp; English.

XX This sequence is calreticulin, a homologue of Clq and collectin receptor  
 (cClqR). The invention relates to the use of a cClqR binding domain in a  
 medicament to effect complement ubiquitin (CUB) functionality, and an  
 inhibitor of the cClqR binding domain in a medicament to inhibit CUB  
 functionality. The cClqR binding domain, or its inhibitor, can be used to  
 treat a human or animal body. Particularly an inhibitor is used to treat  
 complement activation involved in the initiation and maintenance of  
 inflammation, for example in myocardial infarction, brain ischaemia  
 (stroke), gut ischaemia, rheumatoid arthritis, systemic lupus  
 erythematosus, burns, immune complex nephritis, and to treat amyloid  
 plaques in Alzheimer's disease. The use of cClqR binding domain or  
 inhibitor enables the CUB domain functionality to be modulated using a  
 low molecular weight molecule.

XX Sequence 417 AA;

Query Match 100.0%; Score 340; DB 20; Length 417;  
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QY 1 TDMHGDSEYNIMFGPDICGPGTKKHVIFNKGKKNVLINKDIRCKDDETHLYTLIVRPD 60  
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QY 61 N 61

Db 180 n 180

RESULT 5

AA092349  
 ID AAY92349 standard; Protein; 417 AA.

XX  
 AC AAY92349;

XX 10-AUG-2000 (first entry)

XX Human MBP-calreticulin.

XX MBP-calreticulin; maltose binding protein; angiogenesis; inhibition;  
 KW endothelial cell; anti-angiogenic; neuroprotective; antidiabetic;  
 KW cytosolic; dermalogical; immunosuppressive; antiinflammatory; hepatic;  
 KW anti-atherosclerotic; gastrointestinal; anti-arthritis; ophthalmic.

XX Homo sapiens.

XX Key Location/Qualifiers  
 FH Peptide 1..17  
 FT /label= signal\_peptide  
 FT Protein 18  
 FT /label= mature\_protein

XX WO200020577-A1.

XX 13-APR-2000.

XX 05-OCT-1999; 99WO-US23240.

XX 06-OCT-1998; 98US-0103438.

XX (USSH ) US DEPT HEALTH & HUMAN SERVICES.

XX Tosato G, Pike SE, Yao L;

XX WPI; 2000-303767/26.

XX N-PSDB; AAA09346, AAA09347.

XX Inhibiting endothelial cell growth and angiogenesis using calreticulin,  
 useful for suppressing tumor growth

XX Disclosure; Page 79-80; 99pp; English.

XX A novel method of inhibiting endothelial cell growth comprises  
 contacting the cells with calreticulin (or its fragments/variants).  
 Fragments of calreticulin causes at least 40% inhibition of angiogenesis,  
 tumor growth and/or endothelial cell growth (claimed). The method may be  
 used for inhibiting angiogenesis in a patient. The angiogenesis is  
 associated with a disease other than a tumor that is associated with  
 neovascularization (e.g. diabetic neuropathy, retrolental fibroplasia,  
 trachoma, neovascular glaucoma, psoriasis, angiofibromas, immune  
 inflammation, atherosclerosis, excessive wound repair, retinal  
 neovascularization, macular degeneration, corneal graft rejection,  
 contact lens overwear, Crohn's disease, non-immune inflammation,  
 rheumatoid arthritis, systemic lupus erythematosus, thyroiditis,  
 Goodpasture's syndrome, systemic vasculitis, scleroderma, Sjorgen's  
 syndrome, sarcoidosis and primary biliary cirrhosis). The method may  
 also be used for treating/inhibiting tumor growth especially  
 Kaposi's sarcoma (claimed).

XX

SQ Sequence 417 AA;

Query Match 100.0%; Score 340; DB 21; Length 417;  
 Best Local Similarity 100.0%; Pred. No. 1.2e-38;  
 Matches 61; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 TDMHGDSEYNIMFGPDICGPGTKKVVHFNKGNVINKDIRCKDDEFTHLYTLIVRPD 60  
 |||||  
 Db 120 tdmhgdsynimfgpdicpgptkvvhfnfykgknvlinkdirckddefthlytlivrp 179  
 QY 61 N 61  
 |  
 Db 180 n 180

RESULT 6

AAW11156  
 ID AAW11156 standard; peptide; 401 AA.

XX AC AAW11156;

XX DT 31-MAY-1997 (first entry)

XX DE Calreticulin.

XX KW calreticulin; C-domain; restenosis; inhibitor.

XX OS Homo sapiens.

XX PN WO9636643-A1.

XX PD 21-NOV-1996.

XX PF 17-MAY-1996; 96WO-IB00471.

XX PR 16-MAY-1996; 96US-0649417.

XX PS 17-MAY-1995; 95US-0442844.

XX PA (UYAL-) UNIV ALBERTA.

XX PI Lucus A, Michalak M;

XX PS WPI; 1997-012036/01.

XX PT Inhibition of restenosis in patients - using calreticulin or a  
 PT C-domain polypeptide of calreticulin or a variant with the same  
 PT activity.

XX PS Disclosure; Fig 1; 48pp; English.

XX CC The present sequence is calreticulin. It and a C-domain derived peptide  
 CC (AAW06736) are useful for treating a patient to inhibit restenosis. The  
 CC calreticulin-type cpds. are administered either parenterally,  
 CC intravenously or via a catheter and can target areas of vascular damage  
 CC to inhibit or prevent restenosis.

XX SQ Sequence 401 AA;

Query Match

Best Local Similarity 98.5%; Score 335; DB 18; Length 401;

Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DMHGDSEYNIMFGPDICGPGTKKVVHFNKGNVINKDIRCKDDEFTHLYTLIVRPD 61  
 |||||

Db 104 dmhgdsynimfgpdicpgptkvvhfnfykgknvlinkdirckddefthlytlivrp 163

RESULT 7

AAW04171

ID AAW04171 standard; Protein; 403 AA.

XX

AC AAW04171;

XX DT 12-DEC-1996 (first entry)

XX DE Flea calreticulin PctCal403.

XX KW Calreticulin; flea; haematophagous insect; allergic dermatitis;

XX OS vaccine; therapy; PctCal403.

XX PN Ctenocephalides felis.

XX PD WO9628469-A1.

XX PF 19-SEP-1996.

XX PR 08-MAR-1996; 96WO-US03133.

XX PS 09-MAR-1995; 95US-0401509.

XX PA (HESK-) HESKA CORP.

XX PI Rushlow KE, Stiegler GL;

XX DR WPI; 1996-442861/44.

XX PS N-PSDB; AAT39516;

XX PS N-PSDB; AAT39517.

XX PT Haematophagous insect calreticulin protein - used to reduce insect  
 PT infestation and desensitise patients to allergic dermatitis

XX PS Claim 5; Page 68-69; 86pp; English.

XX CC Flea calreticulin protein PctCal1589 (AAW04171) is a calcium-binding  
 CC protein found in the salivary glands of Ctenocephalides felis.  
 CC Its amino acid sequence was deduced from a cDNA clone (AAT39516)  
 CC obt'd. from a salivary gland cDNA library. Recombinant PctCal1589  
 CC can be produced in host cells transformed with a vector carrying  
 CC calreticulin nucleic acids. Calreticulin alters the blood feeding  
 CC behaviour of haematophagous insects and can be administered to an  
 CC animal to reduce infestation. It reduces calreticulin activity in  
 CC insects, so reducing the insect burden on an animal. Calreticulin  
 CC can be used to elicit an immune response, thereby desensitising an  
 CC animal to allergic dermatitis caused by fleas, mosquitoes or  
 CC Culicoides.

XX SQ Sequence 403 AA;

Query Match 85.3%; Score 290; DB 17; Length 403;

Best Local Similarity 83.3%; Pred. No. 9.8e-32;

Matches 50; Conservative 6; Mismatches 4; Indels 0; Gaps 0;

QY 2 DMHGDSEYNIMFGPDICGPGTKKVVHFNKGNVINKDIRCKDDEFTHLYTLIVRPD 61  
 |||||

Db 121 dmhgdsynimfgpdicpgptkvvhfnfykgknvlinkdirckddefthlytlivrp 180

RESULT 8

AAAR12312

ID AAR12312 standard; Protein; 336 AA.

XX AC AAR12312;

XX DT 29-AUG-1991 (first entry)

XX DE Partial sequence of Onchocera volvulus 42 kD antigen.

XX KW River blindness; onchocerciasis; vaccine; antigen; parasite.

XX OS Onchocerca volvulus.

XX PS Key Region

XX PS Location/Qualifiers  
 160..166

[illegible]







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RESULT 15  
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XX  
AC AAG47933;  
XX  
DT 18-OCT-2000 (first entry)  
XX  
DE Arabidopsis thaliana protein fragment SEQ ID NO: 60470.  
XX  
KW Protein identification; signal transduction pathway; metabolic pathway;  
KW hybridisation assay; genetic mapping; gene expression control; promoter;  
KW termination sequence.  
XX  
OS Arabidopsis thaliana.  
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PR 26-OCT-1999; 99US-0161360.  
PR 26-OCT-1999; 99US-0161361.  
PR 28-OCT-1999; 99US-0161920.  
PR 28-OCT-1999; 99US-0161992.  
PR 28-OCT-1999; 99US-0161993.  
PR 29-OCT-1999; 99US-0162142.

Query Match 57.1%; Score 194; DB 21; Length 312;  
Best Local Similarity 60.7%; Pred. No. 1.4e-18;  
Matches 34; Conservative 7; Mismatches 15; Indels 0; Gaps 0;  
QY 5 GDSEYIMFGPDICGPGTKGVIFNYKGNVLINKDIRCKDDEFTHLYTLIVRPD 60  
DB 15 9dtpysimfgpdicgystkvhailtyneanhlkkdvpcetdqlchvytfilrpd 70

Search completed: January 9, 2002, 15:01:12  
Job time: 158 sec

GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: January 9, 2002, 14:59:42 ; Search time 38.34 Seconds  
(without alignments)  
35.803 Million cell updates/sec

Title: US-09-828-000-4  
Perfect score: 340  
Sequence: 1 TMHGDSEYNMFGPDICGP.....IRCKDDEFTHLYTLVIRPDN 61

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 212252 seqs, 22503292 residues

Total number of hits satisfying chosen parameters: 212252

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	202	59.4	415	4	US-08-675-816-2
2	125.5	36.9	542	4	US-08-675-816-6
3	120.5	35.4	593	1	US-08-296-362-2
4	58	17.1	250	1	US-08-378-761A-78
5	58	17.1	250	1	US-08-485-286-78
6	58	17.1	263	1	US-07-901-707-7
7	58	17.1	263	1	US-07-988-430-7
8	58	17.1	263	1	US-08-425-336-7
9	58	17.1	263	1	US-08-488-113B-7
10	58	17.1	263	1	US-08-477-484B-7
11	58	17.1	263	2	US-08-646-360-7
12	58	17.1	263	4	US-08-839-765-7
13	58	17.1	263	4	US-09-136-389-7
14	58	17.1	263	5	PCT-US92-09487-7
15	56	16.5	319	3	US-09-100-664A-10
16	56	16.5	1492	4	US-09-687-898-4
17	55.5	16.3	236	1	US-08-307-499-28
18	55.5	16.3	236	4	US-09-299-268-28
19	54.5	16.0	992	1	US-07-813-593-2
20	54.5	16.0	992	1	US-07-977-451-2
21	54.5	16.0	992	1	US-07-946-507-2
22	54.5	16.0	992	1	US-08-252-517-2
23	54.5	16.0	992	1	US-07-906-397A-2
24	54.5	16.0	992	1	US-08-601-891-2
25	54.5	16.0	992	2	US-09-021-324-2
26	54.5	16.0	992	5	PCT-US92-02750-2
27	54.5	16.0	992	5	PCT-US92-05401-2

28	54.5	16.0	992	5	PCT-US92-09893-2	Sequence 2, Appli
29	54.5	16.0	1000	1	US-08-222-299-2	Sequence 2, Appli
30	54.5	16.0	1000	2	US-08-434-878-2	Sequence 2, Appli
31	54.5	16.0	1000	5	PCT-US95-03718-2	Sequence 2, Appli
32	54	15.9	149	3	US-08-836-236-9	Sequence 9, Appli
33	53.5	15.7	505	2	US-08-394-189B-5	Sequence 5, Appli
34	53.5	15.7	505	5	PCT-US93-05701-20	Sequence 20, Appli
35	53.5	15.7	505	5	PCT-US93-05705-5	Sequence 5, Appli
36	53	15.6	325	1	US-08-447-500-8	Sequence 8, Appli
37	53	15.6	325	1	US-08-454-097-8	Sequence 8, Appli
38	53	15.6	325	1	US-08-453-866-8	Sequence 8, Appli
39	53	15.6	325	3	US-08-185-359-8	Sequence 8, Appli
40	53	15.6	337	1	US-08-447-500-10	Sequence 10, Appli
41	53	15.6	337	1	US-08-454-097-12	Sequence 12, Appli
42	53	15.6	337	1	US-08-453-866-10	Sequence 10, Appli
43	53	15.6	337	3	US-09-100-664A-11	Sequence 11, Appli
44	53	15.6	337	3	US-09-100-664A-12	Sequence 12, Appli
45	53	15.6	337	3	US-08-185-359-12	Sequence 12, Appli

ALIGNMENTS

RESULT 1  
US-08-675-816-2  
; Sequence 2, Application US/08675816  
; Patent No. 6171864  
; GENERAL INFORMATION:  
; APPLICANT: Coughlan, Sean J.  
; APPLICANT: Winfrey, Jr., Ron J.  
; TITLE OF INVENTION: CALRETICULIN AND CALNEXIN GENES AND PROMOTER REGIONS AND US  
; NUMBER OF SEQUENCES: 16  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Seed and Berry  
; STREET: 701 Fifth Ave. Suite 6300  
; CITY: Seattle  
; STATE: Washington  
; COUNTRY: U.S.A.  
; ZIP: 98104-7092  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/675,816  
; FILING DATE: 05-JUL-1996  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: No. 6171864tenburg, Carol  
; REGISTRATION NUMBER: 39,317  
; REFERENCE/DOCKET NUMBER: 750027.401  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (206)-622-4900  
; TELEFAX: (206)-682-6031  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 415 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-675-816-2

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Best Local Similarity 60.7%; Pred. No. 3.7e-19;  
Matches 34; Conservative 9; Mismatches 13; Indels 0; Gaps 0;

QY 5 GDSEYNMFGPDICGPTGKVKHVIENYKKNVLIINKDIRCKDDEFTHLYTLVIRPD 60  
DB 125 GDTPTSIMFGPDICGYSKKVHAILNYNDTNHLIKKEVPCETDQLTHLYTLVIRPD 180



[illegible]

Mat  
Mat  
TITLE OF INVENTION: Mat

APPLICANT: Lei, Shau-ping

; TITLE OF INVENTION: Materials

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; TITLE OF INVENTION: Preparation and Use for Ribosome-Inactivating Proteins
; NUMBER OF SEQUENCES: 101
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Marshall, O'Toole, Gerstein, Murray &
; ADDRESSER: Bicknell
; STREET: Two First National Plaza, 20 South Clark
; STREET: Street
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60603
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION NUMBER: US/07/988,430
; APPLICATION NUMBER: US/07/988,430
; FILING DATE: 19921209
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/901,707
; FILING DATE: 19-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/787,567
; FILING DATE: 04-NOV-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 5416202and, Greta E.
; REGISTRATION NUMBER: 35302
; REFERENCE/DOCKET NUMBER: 31133
; TELEPHONE: (312) 346-5750
; TELEFAX: (312) 984-9740
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 263 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; UN-07-988-430-7

Query Match 17.1%; Score 58; DB 1; Length 263;
Best Local Similarity 29.2%; Pred. No. 4.5;
Matches 14; Conservative 10; Mismatches 16; Indels 8; Gaps 2;

QY 9 YNI-MFGPDICGPGTKKHVIFNYKGNVLLINKDIRCKDDEFTHTL 55
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Db 32 YNIPLLPVSAGRYLLMHLFNYDGKTTTVAADV-----TNVYIM 72

RESULT 8
US-08-425-336-7
; Sequence 7, Application US/08425336
; Patent No. 5621083
; GENERAL INFORMATION:
; APPLICANT: Better, Marc D.
; APPLICANT: Carroll, Stephen F.
; APPLICANT: Studnika, Gary M.
; TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
; TITLE OF INVENTION: Proteins
; NUMBER OF SEQUENCES: 140
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible

; TITLE OF INVENTION: Preparation and Use for Ribosome-Inactivating Proteins
; NUMBER OF SEQUENCES: 101
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Marshall, O'Toole, Gerstein, Murray &
; ADDRESSER: Bicknell
; STREET: Two First National Plaza, 20 South Clark
; STREET: Street
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60603
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION NUMBER: US/07/988,430
; APPLICATION NUMBER: US/07/988,430
; FILING DATE: 19921209
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/901,707
; FILING DATE: 19-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/787,567
; FILING DATE: 04-NOV-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Meyers, Thomas C.
; REGISTRATION NUMBER: P-36,989
; REFERENCE/DOCKET NUMBER: 31394
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/474-6300
; TELEFAX: 312/474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 263 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-425-336-7

Query Match 17.1%; Score 58; DB 1; Length 263;
Best Local Similarity 29.2%; Pred. No. 4.5;
Matches 14; Conservative 10; Mismatches 16; Indels 8; Gaps 2;

QY 9 YNI-MFGPDICGPGTKKHVIFNYKGNVLLINKDIRCKDDEFTHTL 55
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Db 32 YNIPLLPVSAGRYLLMHLFNYDGKTTTVAADV-----TNVYIM 72

RESULT 9
US-08-488-113B-7
; Sequence 7, Application US/08488113B
; Patent No. 5744580
; GENERAL INFORMATION:
; APPLICANT: Better, Marc D.
; APPLICANT: Carroll, Stephen F.
; APPLICANT: Studnika, Gary M.
; TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
; TITLE OF INVENTION: Proteins
; NUMBER OF SEQUENCES: 169
; CORRESPONDENCE ADDRESS:
; ADDRESSER: McAndrews, Held & Malloy, Ltd.
; STREET: 500 West Madison Street, 34th floor
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60661
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/488,113B
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/425,336
; FILING DATE: 18-APR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/064,691
; FILING DATE: 12-MAY-1993
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RESULT 11
US-08-646-360-7
: Sequence 7, Application US/08646360
: Patent No. 5837491
: GENERAL INFORMATION:
: APPLICANT: Better, Marc D.
: APPLICANT: Carroll, Stephen F.
: APPLICANT: Studnika, Gary M.
: TITLE OF INVENTION: Immunotoxins Comprising Ribotoxins
: TITLE OF INVENTION: Proteins
: NUMBER OF SEQUENCES: 173
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: McAndrews, Heid & Malloy, Ltd.
: STREET: 500 West Madison Street, 34th floor
: CITY: Chicago
: STATE: Illinois
: COUNTRY: USA
: ZIP: 60661
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/646,360
: FILING DATE: 13-MAY-1996
: CLASSIFICATION: 530
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: PCT/US94/05348
: FILING DATE: 12-MAY-1994
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/064,691
: FILING DATE: 12-MAY-1993
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 07/988,430
: FILING DATE: 09-DEC-1992
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 07/901,707
: FILING DATE: 19-JUN-1992
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 07/787,567
: FILING DATE: 04-NOV-1991
: ATTORNEY/AGENT INFORMATION:

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Query Match 17.1%; Score 58; DB 4; Length 263;  
Best Local Similarity 29.2%; Pred. No. 4.5;  
Matches 14: Conservative 10. Mismatches 16. Indels

Query Match	17.1%	Score 58;	DB 4;	Length 263;
Best Local Similarity	29.2%	Pred. NO. 4.5;		
Matches	14: Conservative	10: Mismatches	16: Indels	8: Gaps

QY 9 YNI-MFGPDICGPGTKKVHVIFNYKGNVLINKDIRCKDDEFTHTL 55  
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 Db 32 YNIPILLPSVSGAGRYLLMHLEFNVDGKTTVAADV-----TNVYIM 72

RESULT 13  
US-09-136-

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: GENERAL INFORMATION:
: APPLICANT: Better, Marc D.
: APPLICANT: Carroll, Stephen F.
: APPLICANT: Studnika, Gary M.
: TITLE OF INVENTION: Immunotoxin
: TITLE OF INVENTION: Proteins
: NUMBER OF SEQUENCES: 173
: CORRESPONDENCE ADDRESS:
:

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ADDRESSEE: McAndrews, Held & Malloy, Ltd.  
STREET: 500 West Madison Street, 34th floor  
CITY: Chicago  
STATE: Illinois  
COUNTRY: USA  
ZIP: 60661

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? COMPUTER READABLE FORM:
? MEDIUM TYPE: Floppy disk
? COMPUTER: IBM PC compatible
? OPERATING SYSTEM: PC-DOS/MS-DOS
? SOFTWARE: PatentIn Release #1.0, Version #1.25
? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: US/09/136,389
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?
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/ CLASSIFICATION:
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 08/646,360
/ FILING DATE: 13-MAY-1996
/ APPLICATION NUMBER: PCT/US94/05348
/ FILING DATE: 12-MAY-1994
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/064,691
/ FILING DATE: 12-MAY-1993
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 07/988,430
/ FILING DATE: 09-DEC-1992

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PRIORITY APPLICATION DATA: US 07/901,707  
 FILING DATE: 19-JUN-1992  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 07/787,567  
 FILING DATE: 04-NOV-1991  
 ATTORNEY/AGENT INFORMATION:  
 NAME: MCNICOLAS, Janet M.  
 REGISTRATION NUMBER: 32,918  
 REFERENCE/DOCKET NUMBER: 200-70-P4  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 312/707-8889  
 TELEFAX: 312/707-9155  
 TELEX: 650 388-1248  
 INFORMATION FOR SFO ID NO: 7:

REGISTRATION NUMBER: 32,918  
REFERENCE/DOCKET NUMBER: 11022US09/200-70.P3.C3  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 312/707-8889

Query Match 17.1%; Score 58; DB 5; Length 263;  
Best Local Similarity 29.2%; Pred. No. 4.5;  
Matches 14; Conservative 10; Mismatches 16; Indels

Search completed: January 9, 2002, 14:59:43  
Job time: 70 sec

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GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: January 9, 2002, 14:59:43 ; Search time 38.34 Seconds  
(without alignments)  
15.847 Million cell updates/sec

Title: US-09-828-000-5  
Perfect score: 151  
Sequence: 1 CGPGTKKHVIFNYKGNVLINKDIRC 27  
Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 212252 seqs, 22503292 residues

Total number of hits satisfying chosen parameters: 212252

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued\_Patents\_AA.\*  
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2: /cgn2\_6/ptodata/2/1aa/5B-COMB.pap.\*  
3: /cgn2\_6/ptodata/2/1aa/6A-COMB.pap.\*  
4: /cgn2\_6/ptodata/2/1aa/6B-COMB.pap.\*  
5: /cgn2\_6/ptodata/2/1aa/PCITUS-COMB.pap.\*  
6: /cgn2\_6/ptodata/2/1aa/backfiles1.pap.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	82	54.3	415	4	US-08-675-816-2
2	49	32.5	593	1	US-08-208-036-17
3	49	32.5	593	1	US-08-428-823-17
4	49	32.5	876	2	US-08-633-476-2
5	49	32.5	877	1	US-08-208-036-14
6	49	32.5	877	1	US-08-428-823-14
7	48	31.8	17	4	US-08-998-679-63
8	48	31.8	17	4	US-08-939-833A-14
9	48	31.8	17	4	US-09-113-395-23
10	48	31.8	17	4	US-09-113-977C-68
11	47	31.1	490	1	US-08-361-611-2
12	47	31.1	490	1	US-08-565-655-2
13	47	31.1	490	2	US-08-946-987-2
14	44.5	29.5	149	3	US-08-836-236-9
15	44	29.1	113	4	US-08-975-762-67
16	44	29.1	113	4	US-09-295-028-67
17	44	29.1	113	4	US-09-106-582-67
18	44	29.1	496	4	US-08-924-183-10
19	44	29.1	496	4	US-09-488-384-10
20	43.5	28.8	351	1	US-08-415-751-18
21	43	28.5	76	2	US-08-117-952-757
22	43	28.5	250	1	US-08-378-761A-78
23	43	28.5	250	1	US-08-485-286-78
24	43	28.5	263	1	US-07-901-707-7
25	43	28.5	263	1	US-07-988-430-7
26	43	28.5	263	1	US-08-425-336-7
27	43	28.5	263	1	US-08-488-113B-7

28	43	28.5	263	1	US-08-477-484B-7	Sequence 7, Appli
29	43	28.5	263	2	US-08-646-360-7	Sequence 7, Appli
30	43	28.5	263	4	US-08-839-765-7	Sequence 7, Appli
31	43	28.5	263	4	US-09-136-389-7	Sequence 7, Appli
32	43	28.5	263	5	PCT-US92-09487-7	Sequence 7, Appli
33	42	27.8	499	2	US-09-032-315-3	Sequence 3, Appli
34	42	27.8	499	2	US-08-993-318A-3	Sequence 3, Appli
35	42	27.8	499	4	US-09-399-886-3	Sequence 3, Appli
36	42	27.8	499	4	US-09-396-260-3	Sequence 3, Appli
37	42	27.8	499	4	US-09-576-281-3	Sequence 3, Appli
38	42	27.8	510	2	US-08-300-584-4	Sequence 4, Appli
39	42	27.8	510	4	US-08-476-123-4	Sequence 4, Appli
40	42	27.8	519	1	US-08-462-484-4	Sequence 4, Appli
41	42	27.8	519	1	US-08-441-147-4	Sequence 4, Appli
42	42	27.8	519	5	PCT-US95-07536-4	Sequence 4, Appli
43	42	27.8	590	4	US-08-743-168B-43	Sequence 43, Appli
44	42	27.8	911	1	US-08-596-985-2	Sequence 2, Appli
45	41	27.2	503	2	US-08-481-337A-2	Sequence 2, Appli

ALIGNMENTS

RESULT 1  
US-08-675-816-2  
; Sequence 2, Application US/08675816  
; Patent No. 6171864  
; GENERAL INFORMATION:  
; APPLICANT: Coughlan, Sean J.  
; TITLE OF INVENTION: CALRETICULIN AND CALNEXIN GENES AND PROMOTER REGIONS AND US  
; NUMBER OF SEQUENCES: 16  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Seed and Berry  
; STREET: 701 Fifth Ave. Suite 6300  
; CITY: Seattle  
; STATE: Washington  
; COUNTRY: U.S.A.  
; ZIP: 98104-7092  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/675,816  
; FILING DATE: 05-JUL-1996  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: No. 6171864tenburg, Carol  
; REGISTRATION NUMBER: 39,317  
; REFERENCE/DOCKET NUMBER: 750027.401  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (206-622-4900  
; TELEFAX: (206)-682-6031  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 415 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-675-816-2

Query Match 54.3%; Score 82; DB 4; Length 415;  
Best Local Similarity 55.6%; Pred. No. 0.00013;  
Matches 15; Conservative 2; Mismatches 10; Indels 0; Gaps 0;

QY 1 CGPGTKKHVIFNYKGNVLINKDIRC 27  
||| ||||| ||| ||| ||| :  
DB 138 CGYSTKKVHALLNYNDTNHLIKKEVPC 164

RESULT 2  
US-08-208-036-17  
; Sequence 17, Application US/08208036  
; Patent No. 5436326  
; GENERAL INFORMATION:  
; APPLICANT: Yoshizumi IISHINO et al.  
; TITLE OF INVENTION: METHOD FOR CLONING OF A GENE FOR POL I TYPE  
; NUMBER OF SEQUENCES: 17  
; CORRESPONDENCE ADDRESS:  
; ADDRESSER: Wenderoth, Lind & Ponack  
; STREET: 805 Fifteenth Street, N.W., #700  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: U.S.A.  
; ZIP: 20005  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette, 5.25 inch, 500 kb  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: MS-DOS  
; SOFTWARE: DisplayWrite  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/208,036  
; FILING DATE:  
; CLASSIFICATION: 435  
; PRIOR APPLICATION NUMBER: US/07/887,282  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Warren M. Cheek, Jr.  
; REGISTRATION NUMBER: 33,367  
; REFERENCE/DOCKET NUMBER:  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202-371-8850  
; TELEFAX:  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 17:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 593 amino acid residues  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; HYPOTHETICAL:  
; ANTI-SENSE:  
; FRAGMENT TYPE:  
; ORIGINAL SOURCE:  
; ORGANISM:  
; STRAIN:  
; INDIVIDUAL ISOLATE:  
; DEVELOPMENTAL STAGE:  
; HAPLOTYPE:  
; TISSUE TYPE:  
; CELL LINE:  
; ORGANELLE:  
; IMMEDIATE SOURCE:  
; LIBRARY:  
; CLONE:  
; POSITION IN GENOME:  
; CHROMOSOME/SEGMENT:  
; MAP POSITION:  
; UNITS:  
; FEATURE:  
; NAME/KEY:  
; LOCATION:  
; IDENTIFICATION METHOD:  
; OTHER INFORMATION:  
; PUBLICATION INFORMATION:  
; AUTHORS:  
; TITLE:  
; JOURNAL:  
; VOLUME:

; ISSUE:  
; PAGES:  
; DATE:  
; DOCUMENT NUMBER:  
; FILING DATE:  
; PUBLICATION DATE:  
; RELEVANT RESIDUES IN SEQ ID NO:  
US-08-208-036-17  
Query Match 32.5%; Score 49; DB 1; Length 593;  
Best Local Similarity 81.8%; Pred. No. 19;  
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 3 PGTKKVHVIFN 13  
| | | | | | | |  
DB 314 PDTKKVHTIFN 324  
RESULT 3  
US-08-428-823-17  
; Sequence 17, Application US/08428823  
; Patent No. 5753482  
; GENERAL INFORMATION:  
; APPLICANT: Yoshizumi IISHINO et al.  
; TITLE OF INVENTION: METHOD FOR CLONING OF A GENE FOR  
; NUMBER OF SEQUENCES: 17  
; CORRESPONDENCE ADDRESS:  
; ADDRESSER: Wenderoth, Lind & Ponack  
; STREET: 805 Fifteenth Street, N.W., #700  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: U.S.A.  
; ZIP: 20005  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: MS-DOS  
; SOFTWARE: WordPerfect 5.1+  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/428,823  
; FILING DATE: April 25, 1995  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Matthew Jacob  
; REGISTRATION NUMBER: 25,154  
; REFERENCE/DOCKET NUMBER:  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202-371-8850  
; TELEFAX:  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 17:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 593 amino acid residues  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; HYPOTHETICAL:  
; ANTI-SENSE:  
; FRAGMENT TYPE:  
; ORIGINAL SOURCE:  
; ORGANISM:  
; STRAIN:  
; INDIVIDUAL ISOLATE:  
; DEVELOPMENTAL STAGE:  
; HAPLOTYPE:  
; TISSUE TYPE:  
; CELL TYPE:

CELL LINE:  
ORGANELLE:  
IMMEDIATE SOURCE:  
LIBRARY:  
CLONE:  
POSITION IN GENOME:  
CHROMOSOME/SEGMENT:  
MAP POSITION:  
UNITS:  
FEATURE:  
NAME/KEY:  
LOCATION:  
IDENTIFICATION METHOD:  
OTHER INFORMATION:  
PUBLICATION INFORMATION:  
AUTHORS:  
TITLE:  
JOURNAL:  
VOLUME:  
ISSUE:  
PAGES:  
DATE:  
DOCUMENT NUMBER:  
FILING DATE:  
PUBLICATION DATE:  
RELEVANT RESIDUES IN SEQ ID NO:

Query Match 32.5%; Score 49; DB 1; Length 593;  
Best Local Similarity 81.8%; Pred. No. 19;  
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 PGTKKVHVIFN 13  
| | | | | | | |  
DB 314 PDTKKVHTFN 324

RESULT 4  
US-08-633-476-2  
; Sequence 2, Application US/08633476  
; Patent No. 5830714  
; GENERAL INFORMATION:  
; APPLICANT: Swaminathan, Neela  
; APPLICANT: Wilkosz, Richard K.  
; APPLICANT: Muller, Reinhold  
; TITLE OF INVENTION: BIOLOGICALLY ACTIVE FRAGMENT OF  
; TITLE OF INVENTION: BACILLUS STEAROTHERMOPHILUS DNA POLYMERASE  
; NUMBER OF SEQUENCES: 5  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun  
; STREET: 6300 Sears Tower, 233 South Wacker Drive  
; CITY: Chicago  
; STATE: Illinois  
; COUNTRY: USA  
; ZIP: 60606-6402  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/633,476  
; FILING DATE:  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Pochoipien, Donald J.  
; REGISTRATION NUMBER: 32,167  
; REFERENCE/DOCKET NUMBER: 28003/32630  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 312/474-6300  
; TELEFAX: 312/474-0448  
; TELEX: 25-3856

; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 876 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-633-476-2

Query Match 32.5%; Score 49; DB 2; Length 876;  
Best Local Similarity 81.8%; Pred. No. 31;  
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 PGTKKVHVIFN 13  
| | | | | | | |  
DB 597 PDTKKVHTFN 607

RESULT 5  
US-08-208-036-14  
; Sequence 14, Application US/08208036  
; Patent No. 5436326  
; GENERAL INFORMATION:  
; APPLICANT: Yoshizumi, IISHINO et al.  
; TITLE OF INVENTION: METHOD FOR CLONING OF A GENE FOR POL I TYPE  
; TITLE OF INVENTION: DNA POLYMERASE  
; NUMBER OF SEQUENCES: 17  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Wenderoth, Lind & Ponack  
; STREET: 805 Fifteenth Street, N.W., #700  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: U.S.A.  
; ZIP: 20005  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette, 5.25 inch, 500 kb  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: MS-DOS  
; SOFTWARE: DisplayWrite  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/208,036  
; FILING DATE:  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/07/887,282  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Warren M. Cheek, Jr.  
; REGISTRATION NUMBER: 33,367  
; REFERENCE/DOCKET NUMBER:  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202-371-8850  
; TELEFAX:  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 14:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 877 amino acid residues  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; HYPOTHETICAL:  
; ANTI-SENSE:  
; FRAGMENT TYPE:  
; ORIGINAL SOURCE:  
; ORGANISM:  
; STRAIN:  
; INDIVIDUAL ISOLATE:  
; DEVELOPMENTAL STAGE:  
; HAPLOTYPE:  
; TISSUE TYPE:  
; CELL TYPE:  
; CELL LINE:

ORGANELLE:  
IMMEDIATE SOURCE:  
LIBRARY:  
CLONE:  
POSITION IN GENOME:  
CHROMOSOME/SEGMENT:  
MAP POSITION:  
UNITS:  
FEATURE:  
NAME/KEY:  
LOCATION:  
IDENTIFICATION METHOD:  
OTHER INFORMATION:  
PUBLICATION INFORMATION:  
AUTHORS:  
TITLE:  
JOURNAL:  
VOLUME:  
ISSUE:  
PAGES:  
DATE:  
DOCUMENT NUMBER:  
FILING DATE:  
PUBLICATION DATE:  
RELEVANT RESIDUES IN SEQ ID NO:  
US-08-208-036-14

Query Match 32.5%; Score 49; DB 1; Length 877;  
Best Local Similarity 81.8%; Pred. No. 31;  
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 PGTKKVHVIFN 13  
DB 598 PDKKVVHTFN 608

## RESULT 6

US-08-428-823-14  
Sequence 14, Application US/08428823  
Patent No. 5753482  
GENERAL INFORMATION:  
APPLICANT: Yoshizumi ISHINO et al.  
TITLE OF INVENTION: METHOD FOR CLONING OF A GENE FOR  
POLYMERASE  
NUMBER OF SEQUENCES: 17  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Wenderoth, Lind & Ponack  
STREET: 805 Fifteenth Street, N.W., #700  
CITY: Washington  
STATE: D.C.  
COUNTRY: U.S.A.  
ZIP: 20005  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: MS-DOS  
SOFTWARE: Wordperfect 5.1+  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/428,823  
FILING DATE: April 25, 1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Matthew Jacob  
REGISTRATION NUMBER: 25,154  
REFERENCE/DOCKET NUMBER:  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-371-8850  
TELEFAX:  
TELEX:

INFORMATION FOR SEQ ID NO: 14:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 877 amino acid residues  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
HYPOTHETICAL:  
ANTI-SENSE:  
FRAGMENT TYPE:  
ORIGINAL SOURCE:  
ORGANISM:  
STRAIN:  
INDIVIDUAL ISOLATE:  
DEVELOPMENTAL STAGE:  
HAPLOTYPE:  
TISSUE TYPE:  
CELL TYPE:  
CELL LINE:  
ORGANELLE:  
IMMEDIATE SOURCE:  
LIBRARY:  
CLONE:  
POSITION IN GENOME:  
CHROMOSOME/SEGMENT:  
MAP POSITION:  
UNITS:

FEATURE:  
NAME/KEY:  
LOCATION:  
IDENTIFICATION METHOD:  
OTHER INFORMATION:  
PUBLICATION INFORMATION:  
AUTHORS:  
TITLE:  
JOURNAL:  
VOLUME:  
ISSUE:  
PAGES:  
DATE:  
DOCUMENT NUMBER:  
FILING DATE:  
PUBLICATION DATE:  
RELEVANT RESIDUES IN SEQ ID NO:  
US-08-428-823-14

Query Match 32.5%; Score 49; DB 1; Length 877;  
Best Local Similarity 81.8%; Pred. No. 31;  
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 PGTKKVHVIFN 13  
DB 598 PDKKVVHTFN 608

## RESULT 7

US-08-996-679-63  
Sequence 63, Application US/08996679  
Patent No. 6169071  
GENERAL INFORMATION:  
APPLICANT: Blaschuk, Orest W.  
APPLICANT: Gour, Barbara J.  
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING  
CELL ADHESION  
NUMBER OF SEQUENCES: 63  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: SEED and BERRY LLP  
STREET: 6300 Columbia Center, 701 Fifth Avenue  
CITY: Seattle  
STATE: Washington  
COUNTRY: USA  
ZIP: 98104



COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA: US/08/996,679  
APPLICATION NUMBER: US/08/996,679  
FILING DATE: 23-DEC-1997  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: Maki, David J.  
REGISTRATION NUMBER: 31,392  
REFERENCE/DOCKET NUMBER: 100086.401C1  
TELEPHONE: (206) 622-4900  
TELEFAX: (206) 682-6031  
INFORMATION FOR SEQ ID NO: 63:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 17 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
US-08-996-679-63

Query Match 31.8%; Score 48; DB 4; Length 17;  
Best Local Similarity 43.8%; Pred. No. 0.43;  
Matches 7; Conservative 7; Mismatches 2; Indels 0; Gaps 0;

QY 11 IFNYGKGNVLINKDIR 26  
I: :||:|:|: ||:|  
Db 1 IWKHGRDVLKKDVR 16

RESULT 8  
US-08-939-853A-14  
; Sequence 14, Application US/08939853A  
; Patent No. 6203788  
; GENERAL INFORMATION:  
; APPLICANT: Blaschuk, Orest W.  
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR REGULATING  
; TITLE OF INVENTION: CELL ADHESION  
; NUMBER OF SEQUENCES: 30  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: SEED and BERRY LLP  
; STREET: 6300 Columbia Center, 701 Fifth Avenue  
; CITY: Seattle  
; STATE: Washington  
; COUNTRY: USA  
; ZIP: 98104  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/939,853A  
FILING DATE: 29-SEP-1997  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Maki, David J.  
REGISTRATION NUMBER: 32,391  
REFERENCE/DOCKET NUMBER: 100086.402  
TELEPHONE: (206) 622-4900  
TELEFAX: (206) 682-6031  
INFORMATION FOR SEQ ID NO: 14:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 17 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear

US-08-939-853A-14

Query Match 31.8%; Score 48; DB 4; Length 17;  
Best Local Similarity 43.8%; Pred. No. 0.43;  
Matches 7; Conservative 7; Mismatches 2; Indels 0; Gaps 0;

QY 11 IFNYGKGNVLINKDIR 26  
I: :||:|:|: ||:|  
Db 1 IWKHGRDVLKKDVR 16

RESULT 9  
US-09-115-395-23  
; Sequence 23, Application US/09115395A  
; Patent No. 6207639  
; GENERAL INFORMATION:  
; APPLICANT: Blaschuk, Orest W.  
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NEURITE OUTGROWTH  
; FILE REFERENCE: 100086.401C3  
; CURRENT APPLICATION NUMBER: US/09/115,395A  
; CURRENT FILING DATE: 1998-07-14  
; EARLIER APPLICATION NUMBER: 08/996,679  
; EARLIER FILING DATE: 1997-12-23  
; EARLIER APPLICATION NUMBER: 08/893,534  
; EARLIER FILING DATE: 1997-07-11  
; EARLIER APPLICATION NUMBER: 60/021,612  
; EARLIER FILING DATE: 1996-07-12  
; NUMBER OF SEQ ID NOS: 77  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 23  
; LENGTH: 17  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Solid Phase  
; OTHER INFORMATION: Synthesis  
US-09-115-395-23

Query Match 31.8%; Score 48; DB 4; Length 17;  
Best Local Similarity 43.8%; Pred. No. 0.43;  
Matches 7; Conservative 7; Mismatches 2; Indels 0; Gaps 0;

QY 11 IFNYGKGNVLINKDIR 26  
I: :||:|:|: ||:|  
Db 1 IWKHGRDVLKKDVR 16

RESULT 10  
US-09-113-977C-68  
; Sequence 68, Application US/09113977C  
; Patent No. 6277824  
; GENERAL INFORMATION:  
; APPLICANT: Doherty, Patrick  
; APPLICANT: Blaschuk, Orest W.  
; APPLICANT: Gour, Barbara J.  
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING ADHESION MOLECULE  
; TITLE OF INVENTION: FUNCTION  
; FILE REFERENCE: 100086.403  
; CURRENT APPLICATION NUMBER: US/09/113,977C  
; CURRENT FILING DATE: 1998-07-10  
; NUMBER OF SEQ ID NOS: 87  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 68  
; LENGTH: 17  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Solid Phase  
; OTHER INFORMATION: Synthesis  
US-09-113-977C-68



Search completed: January 9, 2002, 14:59:44  
Job time: 71 sec

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GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: January 9, 2002, 14:59:44 ; Search time 38.34 Seconds  
(without alignments)  
10.565 Million cell updates/sec

Title: US-09-828-000-6  
Perfect score: 96  
Sequence: 1 VIFYKGNVLINKDIRC 18

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 212252 seqs, 22503292 residues

Total number of hits satisfying chosen parameters: 212252

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	48	50.0	17	4	US-08-996-679-63
2	48	50.0	17	4	US-08-939-853A-14
3	48	50.0	17	4	US-09-113-395-23
4	48	50.0	17	4	US-09-113-977C-68
5	44	45.8	496	4	US-08-924-183-10
6	44	45.8	496	4	US-09-488-364-10
7	43	44.8	76	2	US-08-117-952-757
8	43	44.8	415	4	US-08-675-816-2
9	41	42.7	250	1	US-08-378-761A-78
10	41	42.7	250	1	US-08-485-286-78
11	41	42.7	263	1	US-07-901-707-7
12	41	42.7	263	1	US-07-988-430-7
13	41	42.7	263	1	US-08-425-336-7
14	41	42.7	263	1	US-08-488-113B-7
15	41	42.7	263	1	US-08-477-484B-7
16	41	42.7	263	2	US-08-646-360-7
17	41	42.7	263	4	US-08-839-765-7
18	41	42.7	263	4	US-09-136-389-7
19	41	42.7	263	5	PCT-US92-09487-7
20	41	42.7	503	2	US-08-481-337A-2
21	41	42.7	503	2	US-08-696-268B-2
22	41	42.7	503	4	US-09-382-256-2
23	41	42.7	503	4	US-09-395-115-2
24	41	42.7	503	5	PCT-US94-11328A-4
25	41	42.7	503	5	PCT-US95-05467-2
26	41	42.7	581	4	US-08-743-168B-40
27	41	42.7	590	4	US-08-743-168B-43

28	40	41.7	31	4	US-08-857-076-15	Sequence 15, Appl
29	40	41.7	378	2	US-08-158-735A-11	Sequence 11, Appl
30	40	41.7	669	2	US-08-357-533A-8	Sequence 8, Appl
31	40	41.7	669	3	US-08-459-009-8	Sequence 8, Appl
32	40	41.7	669	3	US-08-459-951-8	Sequence 8, Appl
33	39	40.6	268	4	US-08-904-284-7	Sequence 7, Appl
34	39	40.6	579	4	US-08-743-168B-36	Sequence 36, Appl
35	39	40.6	777	2	US-08-231-193A-16	Sequence 16, Appl
36	39	40.6	777	2	US-08-486-273A-16	Sequence 16, Appl
37	39	40.6	777	3	US-08-480-474-16	Sequence 16, Appl
38	39	40.6	777	3	US-08-940-086A-16	Sequence 16, Appl
39	39	40.6	854	2	US-08-231-193A-32	Sequence 32, Appl
40	39	40.6	854	2	US-08-486-273A-32	Sequence 32, Appl
41	39	40.6	854	3	US-08-480-474-32	Sequence 32, Appl
42	39	40.6	854	3	US-08-940-086A-32	Sequence 32, Appl
43	39	40.6	863	4	US-08-436-332B-2	Sequence 2, Appl
44	39	40.6	870	2	US-08-231-193A-30	Sequence 30, Appl
45	39	40.6	870	2	US-08-486-273A-30	Sequence 30, Appl

ALIGNMENTS

RESULT 1  
US-08-996-679-63  
; Sequence 63, Application US/08996679  
; Patent No. 6169071  
; GENERAL INFORMATION:  
; APPLICANT: Blaschuk, Orest W.  
; APPLICANT: Gour, Barbara J.  
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING CELL ADHESION  
; NUMBER OF SEQUENCES: 63  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: SEED and BERRY LLP  
; STREET: 6300 Columbia Center, 701 Fifth Avenue  
; CITY: Seattle  
; STATE: Washington  
; COUNTRY: USA  
; ZIP: 98104  
; COMPUTER READABLE FORM:  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/996,679  
; FILING DATE: 23-DEC-1997  
; CLASSIFICATION:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Maki, David J.  
; REGISTRATION NUMBER: 31,392  
; REFERENCE/DOCKET NUMBER: 100086.401C1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (206) 622-4900  
; TELEFAX: (206) 682-6031  
; INFORMATION FOR SEQ ID NO: 63:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 17 amino acids  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: linear  
US-08-996-679-63

Query Match 50.0%; Score 48; DB 4; Length 17;  
Best Local Similarity 43.8%; Pred. No. 0.072;  
Matches 7; Conservative 7; Mismatches 2; Indels 0; Gaps 0;

QY 2 IFNYKGNVLINKDIR 17

Db 1 IWKHGRDVLKKDVR 16

10

RESULT 9  
US-08-378-761A-78  
; Sequence 78, Application US/08378761A  
; Patent NO. 5635384  
; GENERAL INFORMATION:

APPLICANT: WALSH, TERENCE A  
APPLICANT: HEY, TIMOTHY D  
APPLICANT: MORGAN, ALICE ER  
TITLE OF INVENTION: RIBOSOME-INACTIVATING PROTEINS, INACTIVE  
TITLE OF INVENTION: PRECURSOR FORMS THEREOF, A PROCESS FOR MAKING A METHOD OF  
TITLE OF INVENTION: USING  
NUMBER OF SEQUENCES: 81  
CORRESPONDENCE ADDRESS:  
ADDRESSER: ANDREA T. BORUCKI  
STREET: 9330 ZIONSVILLE ROAD  
CITY: INDIANAPOLIS  
STATE: IN  
COUNTRY: US  
ZIP: 46268  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/378,761A  
FILING DATE: 26-JAN-1995  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: BORUCKI, ANDREA T  
REGISTRATION NUMBER: 33651  
REFERENCE/DOCKET NUMBER: 38272B  
TELEPHONE: (317) 337-4846  
INFORMATION FOR SEQ ID NO: 78  
SEQUENCE CHARACTERISTICS:  
LENGTH: 250 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-378-761A-78

Query Match 42.7%; Score 41; DB 1; Length 250;  
Best Local Similarity 40.0%; Pred. No. 23;  
Matches 6; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 2 IFNYGKKNVLINKDI 16  
:|||||: : : :  
Db 52 LFNYDGKTTTVAVDV 66

RESULT 10  
US-08-485-286-78  
Sequence 78, Application US/08485286  
Patent No. 5646026  
Patent No. 5646026 5646119  
GENERAL INFORMATION:  
APPLICANT: WALSH, TERENCE A  
APPLICANT: HEY, TIMOTHY D  
APPLICANT: MORGAN, ALICE ER  
TITLE OF INVENTION: RIBOSOME-INACTIVATING PROTEINS, INACTIVE  
TITLE OF INVENTION: PRECURSOR FORMS THEREOF, A PROCESS FOR MAKING A METHOD OF  
TITLE OF INVENTION: USING  
NUMBER OF SEQUENCES: 81  
CORRESPONDENCE ADDRESS:  
ADDRESSER: ANDREA T. BORUCKI  
STREET: 9330 ZIONSVILLE ROAD  
CITY: INDIANAPOLIS  
STATE: IN  
COUNTRY: US  
ZIP: 46268  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/485,286  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/378761  
FILING DATE: 26-JAN-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: BORUCKI, ANDREA T  
REGISTRATION NUMBER: 33651  
REFERENCE/DOCKET NUMBER: 38272B  
TELEPHONE: (317) 337-4846  
INFORMATION FOR SEQ ID NO: 78  
SEQUENCE CHARACTERISTICS:  
LENGTH: 250 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-485-286-78

Query Match 42.7%; Score 41; DB 1; Length 250;  
Best Local Similarity 40.0%; Pred. No. 23;  
Matches 6; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 2 IFNYGKKNVLINKDI 16  
:|||||: : : :  
Db 52 LFNYDGKTTTVAVDV 66

RESULT 11  
US-07-901-707-7  
Sequence 7, Application US/07901707  
Patent No. 5376546  
GENERAL INFORMATION:  
APPLICANT: Bernhard, Susan L.  
APPLICANT: Better, Marc D.  
APPLICANT: Carroll, Steve F.  
APPLICANT: Lane, Julie A.  
TITLE OF INVENTION: Materials Comprising and Methods of  
TITLE OF INVENTION: Composition and Use for Ribosome-Inactivating Proteins  
NUMBER OF SEQUENCES: 57  
CORRESPONDENCE ADDRESS:  
ADDRESSER: Marshall, O'Toole, Gerstein, Murray &  
STREET: Two First National Plaza, 20 South Clark  
STREET: Street  
CITY: Chicago  
STATE: Illinois  
COUNTRY: USA  
ZIP: 60603  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/901,707  
FILING DATE: 19920619  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/787,567  
FILING DATE: 04-NOV-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: No. 5376546and, Greta E.  
REGISTRATION NUMBER: 35,302  
REFERENCE/DOCKET NUMBER: 27129/30910  
TELEPHONE: (312) 346-5750  
TELEFAX: (312) 984-5750  
TELEX: 25-3856



INFORMATION FOR SEQ ID NO: 7:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 263 amino acids  
TYPE: AMINO ACID  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-07-901-707-7

Query Match 42.7%; Score 41; DB 1; Length 263;  
Best Local Similarity 40.0%; Pred. No. 25;  
Matches 6; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 2 IFNYGKGNVLINKDI 16  
Db 52 LFNYDGKTTTVAVDV 66

RESULT 12  
US-07-988-430-7  
Sequence 7, Application US/07988430  
Patent No. 5416202  
GENERAL INFORMATION:  
APPLICANT: Bernhardt, Susan L.  
APPLICANT: Better, Marc D.  
APPLICANT: Carroll, Stephen F.  
APPLICANT: Lane, Julie A.  
APPLICANT: Lei, Shau-Ping  
TITLE OF INVENTION: Materials Comprising and Methods of Preparation and Use for Ribosome-Inactivating Proteins  
TITLE OF INVENTION: Preparation and Use for Ribosome-Inactivating Proteins  
NUMBER OF SEQUENCES: 101  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Bicknell  
STREET: Two First National Plaza, 20 South Clark Street  
CITY: Chicago  
STATE: Illinois  
COUNTRY: USA  
ZIP: 60603  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC Compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/988,430  
FILING DATE: 19921209  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/901,707  
FILING DATE: 19-JUN-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/787,567  
FILING DATE: 04-NOV-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: No. 5416202and, Greta E.  
REGISTRATION NUMBER: 35302  
REFERENCE/DOCKET NUMBER: 31133  
TELEPHONE: (312) 346-5750  
TELEFAX: (312) 984-9740  
TELEX: 25-3856  
INFORMATION FOR SEQ ID NO: 7:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 263 amino acids  
TYPE: AMINO ACID  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-07-988-430-7

Query Match 42.7%; Score 41; DB 1; Length 263;

Best Local Similarity 40.0%; Pred. No. 25;  
Matches 6; Conservative 4; Mismatches 5; Indels 0; Gaps 0;  
QY 2 IFNYGKGNVLINKDI 16  
Db 52 LFNYDGKTTTVAVDV 66

RESULT 13  
US-08-425-336-7  
Sequence 7, Application US/08425336  
Patent No. 5621083  
GENERAL INFORMATION:  
APPLICANT: Better, Marc D.  
APPLICANT: Carroll, Stephen F.  
APPLICANT: Studnika, Gary M.  
TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating  
TITLE OF INVENTION: Proteins  
NUMBER OF SEQUENCES: 140  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun  
STREET: 6300 Sears Tower, 233 South Wacker Drive  
CITY: Chicago  
STATE: Illinois  
COUNTRY: USA  
ZIP: 60606-6402  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC Compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/425,336  
FILING DATE: 18-APR-1995  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/064,691  
FILING DATE: 12-MAY-1993  
APPLICATION NUMBER: US 07/901,707  
FILING DATE: 19-JUN-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/787,567  
FILING DATE: 04-NOV-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Meyers, Thomas C.  
REGISTRATION NUMBER: P-36,989  
REFERENCE/DOCKET NUMBER: 31394  
TELEPHONE: 312/474-6300  
TELEFAX: 312/474-0448  
TELEX: 25-3856  
INFORMATION FOR SEQ ID NO: 7:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 263 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-425-336-7

Query Match 42.7%; Score 41; DB 1; Length 263;  
Best Local Similarity 40.0%; Pred. No. 25;  
Matches 6; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 2 IFNYGKGNVLINKDI 16  
Db 52 LFNYDGKTTTVAVDV 66

RESULT 14  
US-08-488-113B-7  
Sequence 7, Application US/08488113B  
Patent No. 5744580

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; GENERAL INFORMATION:
; APPLICANT: Better, Marc D.
; APPLICANT: Carroll, Stephen F.
; APPLICANT: Studnika, Gary M.
; TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
; NUMBER OF SEQUENCES: 169
; CORRESPONDENCE ADDRESS:
; ADDRESSER: McAndrews, Held & Malloy, Ltd.
; STREET: 500 West Madison Street, 34th floor
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60661
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/488,113B
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/425,336
; FILING DATE: 18-APR-1995
; APPLICATION NUMBER: US 08/064,691
; FILING DATE: 12-MAY-1993
; APPLICATION NUMBER: US 07/988,430
; FILING DATE: 09-DEC-1992
; APPLICATION NUMBER: US 07/901,707
; FILING DATE: 19-JUN-1992
; APPLICATION NUMBER: US 07/787,567
; FILING DATE: 04-NOV-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: McNicholas, Janet M.
; REGISTRATION NUMBER: 32,918
; REFERENCE/DOCKET NUMBER: 11022US07/200-70.P3.C2A
; TELEPHONE: 312/707-8889
; TELEFAX: 312/707-9155
; TELEX: 650 388-1248
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 263 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-488-113B-7

Query Match 42.7%; Score 41; DB 1; Length 263;
Best Local Similarity 40.0%; Pred. No. 25;
Matches 6; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 2 IFNYKGKVNLIKDI 16
Db 52 LFNYDGKTTTVAVDV 66

RESULT 15
US-08-477-484B-7
; Sequence 7, Application US/08477484B
; Patent No. 5756699
; GENERAL INFORMATION:
; APPLICANT: Better, Marc D.
; APPLICANT: Carroll, Stephen F.
; APPLICANT: Studnika, Gary M.
; TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating

```

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; TITLE OF INVENTION: Proteins
; NUMBER OF SEQUENCES: 169
; CORRESPONDENCE ADDRESS:
; ADDRESSER: McAndrews, Held & Malloy, Ltd.
; STREET: 500 West Madison Street, 34th floor
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60661
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/477,484B
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/425,336
; FILING DATE: 18-APR-1995
; APPLICATION NUMBER: US 08/064,691
; FILING DATE: 12-MAY-1993
; APPLICATION NUMBER: US 07/988,430
; FILING DATE: 09-DEC-1992
; APPLICATION NUMBER: US 07/901,707
; FILING DATE: 19-JUN-1992
; APPLICATION NUMBER: US 07/787,567
; FILING DATE: 04-NOV-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: McNicholas, Janet M.
; REGISTRATION NUMBER: 32,918
; REFERENCE/DOCKET NUMBER: 11022US07/200-70.P3.C2A
; TELEPHONE: 312/707-8889
; TELEFAX: 312/707-9155
; TELEX: 650 388-1248
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 263 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-477-484B-7

Query Match 42.7%; Score 41; DB 1; Length 263;
Best Local Similarity 40.0%; Pred. No. 25;
Matches 6; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 2 IFNYKGKVNLIKDI 16
Db 52 LFNYDGKTTTVAVDV 66

Search completed: January 9, 2002, 14:59:44
Job time: 71 sec

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GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: January 9, 2002, 14:59:44 ; Search time 38.34 Seconds  
(without alignments)  
20.543 Million cell updates/sec

Title: US-09-828-000-7  
Perfect score: 189  
Sequence: 1 VIFNYKGNVLINKDIRCKDDEFTHLTVLRPDN 35

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 212252 seqs, 22503292 residues

Total number of hits satisfying chosen parameters: 212252

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued\_Patents\_AA:\*  
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2: /cgn2\_6/ptodata/2/laa/5B\_COMB.pep:\*  
3: /cgn2\_6/ptodata/2/laa/6A\_COMB.pep:\*  
4: /cgn2\_6/ptodata/2/laa/6B\_COMB.pep:\*  
5: /cgn2\_6/ptodata/2/laa/PCTUS\_COMB.pep:\*  
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	105	55.6	415	4	US-08-675-816-2
2	63	33.3	593	1	US-08-296-362-2
3	58	30.7	542	4	US-08-675-816-6
4	50.5	26.7	236	1	US-08-307-499-28
5	50.5	26.7	236	4	US-09-299-268-28
6	48	25.4	17	4	US-08-996-679-63
7	48	25.4	17	4	US-08-939-853A-14
8	48	25.4	17	4	US-09-115-395-23
9	48	25.4	17	4	US-09-113-977C-68
10	47	24.9	599	1	US-08-752-238-3
11	47	24.9	599	3	US-09-085-603B-3
12	47	24.9	599	4	US-09-031-897-7
13	47	24.9	599	4	US-09-257-770-6
14	46.5	24.6	582	3	US-08-906-865-3
15	46	24.3	410	4	US-09-352-990-16
16	45.5	24.1	362	3	US-08-513-974B-374
17	45	23.8	355	1	US-08-292-549-6
18	45	23.8	355	4	US-09-006-353A-14
19	44.5	23.5	129	3	US-08-513-974B-327
20	44	23.3	279	2	US-08-701-191A-23
21	44	23.3	400	4	US-09-352-990-18
22	44	23.3	490	2	US-08-673-789-13
23	44	23.3	496	4	US-08-924-183-10
24	44	23.3	496	4	US-09-488-364-10
25	44	23.3	639	1	US-08-466-390-2
26	44	23.3	639	1	US-08-470-950-2
27	44	23.3	639	1	US-08-467-781-2

28	44	23.3	639	1	US-08-195-487-2	Sequence 2, Appli
29	44	23.3	639	2	US-08-483-924-2	Sequence 2, Appli
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31	44	23.3	710	1	US-08-162-809-22	Sequence 22, Appli
32	44	23.3	722	1	US-08-162-809-4	Sequence 4, Appli
33	44	23.3	744	1	US-08-162-809-20	Sequence 20, Appli
34	44	23.3	816	1	US-08-190-802A-54	Sequence 54, Appli
35	44	23.3	816	4	US-08-477-346-54	Sequence 54, Appli
36	44	23.3	877	2	US-08-673-789-2	Sequence 2, Appli
37	44	23.3	928	1	US-08-442-248-2	Sequence 2, Appli
38	44	23.3	928	1	US-08-440-815-2	Sequence 2, Appli
39	44	23.3	928	4	US-08-486-449-2	Sequence 2, Appli
40	44	23.3	967	2	US-08-449-645A-30	Sequence 30, Appli
41	44	23.3	967	2	US-08-702-367A-30	Sequence 30, Appli
42	44	23.3	982	2	US-08-673-789-4	Sequence 4, Appli
43	44	23.3	983	1	US-08-162-809-16	Sequence 16, Appli
44	44	23.3	983	1	US-08-167-919A-10	Sequence 10, Appli
45	44	23.3	983	2	US-08-449-645A-21	Sequence 21, Appli

ALIGNMENTS

RESULT 1  
US-08-675-816-2  
; Sequence 2, Application US/08675816  
; Patent No. 6171864  
; GENERAL INFORMATION:  
; APPLICANT: Coughlan, Sean J.  
; APPLICANT: Winfrey, Jr., Ron J.  
; TITLE OF INVENTION: CALRETICULIN AND CALNEXIN GENES AND PROMOTER REGIONS AND US  
; NUMBER OF SEQUENCES: 16  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Seed and Berry  
; STREET: 701 Fifth Ave. Suite 6300  
; CITY: Seattle  
; STATE: Washington  
; COUNTRY: U.S.A.  
; ZIP: 98104-7092  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/675,816  
; FILING DATE: 05-JUL-1996  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: No. 6171864tenburg, Carol  
; REGISTRATION NUMBER: 39,317  
; REFERENCE/DOCKET NUMBER: 750027.401  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (206-622-4900  
; TELEFAX: (206)-682-6031  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 415 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-675-816-2

Query Match 55.6%; Score 105; DB 4; Length 415;  
Best Local Similarity 51.5%; Pred. No. 4.4e-08;  
Matches 17; Conservative 7; Mismatches 9; Indels 0; Gaps 0;

QY 2 IFNYKGNVLINKDIRCKDDEFTHLTVLRPD 34

Db 148 ILNNTDTHNHLIKKEVPCETDQTHVTLVIRPD 180

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RESULT 2
US-08-296-362-2
; Sequence 2, Application US/08296362
; Patent No. 5691306
; GENERAL INFORMATION:
; APPLICANT: Bergeron, John J.M.
; APPLICANT: Thomas, David Y.
; APPLICANT: Wada, Ikuro
; TITLE OF INVENTION: METHODS OF DETECTION AND TREATMENT OF
; TITLE OF INVENTION: PROTEIN TRAFFICKING DISORDERS AND INCREASING SECRETORY
; TITLE OF INVENTION: PROTEIN PRODUCTION
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED AND BERRY
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: US
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION NUMBER: US/08/296,362
; FILING DATE: 25-AUG-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: DeVhr, Manya S.
; REGISTRATION NUMBER: 37,120
; REFERENCE/DOCKET NUMBER: 690066.401C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 522-4900
; TELEFAX: (206) 682-6031
; TELEX: 3723836
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 593 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-296-362-2

Query Match 33.3%; Score 63; DB 1; Length 593;
Best Local Similarity 34.1%; Pred. No. 0.16;
Matches 15; Conservative 6; Mismatches 13; Indels 10; Gaps 1;

QY 2 IFNYGKNVLIINKDIRCK-----DDEFTHTLTVLRPN 35
||.||.:.:|
|:|||||:|
DB 204 IFRHKPKYGVYEKHKRPDADLKTYFTDKKTHLTVLRPN 247

RESULT 3
US-08-675-816-6
; Sequence 6, Application US/08675816
; Patent No. 6171864
; GENERAL INFORMATION:
; APPLICANT: Coughlan, Sean J.
; APPLICANT: Winfrey, Jr., Ron J.
; TITLE OF INVENTION: CALRETICULIN AND CALNEXIN GENES AND PROMOTER REGIONS AND USES
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Seed and Berry
; STREET: 701 Fifth Ave. Suite 6300
; CITY: Seattle
; STATE: Washington
; COUNTRY: U.S.A.
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
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; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION NUMBER: US/08/675,816
; FILING DATE: 05-JUL-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 6171864tenburg, Carol
; REGISTRATION NUMBER: 39,317
; REFERENCE/DOCKET NUMBER: 750027.401
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206)-622-4900
; TELEFAX: (206)-682-6031
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 542 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-675-816-6

Query Match 30.7%; Score 58; DB 4; Length 542;
Best Local Similarity 60.0%; Pred. No. 0.85;
Matches 9; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 21 DEFTHTLTVLRPN 35
|:|||||:|
DB 181 DKLTHVYTAILKPDN 195

RESULT 4
US-08-307-499-28
; Sequence 28, Application US/08307499
; Patent No. 5651972
; GENERAL INFORMATION:
; APPLICANT: Moyer, Richard W.
; APPLICANT: Vi uela, Eladio
; APPLICANT: Gibbs, E.P.J.
; TITLE OF INVENTION: Use of Recombinant Swine Poxvirus as a
; TITLE OF INVENTION: Live Vaccine Vector
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: David R. Saliwanchik
; STREET: 2421 N.W. 41st Street, Suite A-1
; CITY: Gainesville
; STATE: Florida
; COUNTRY: U.S.A.
; ZIP: 32606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION NUMBER: US/08/307,499
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/908,241
; FILING DATE: 1-JUL-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/908,630
; FILING DATE: 29-JUN-1992
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/342,212
; FILING DATE: 21-APR-1992
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Saliwanchik, David R.
; REGISTRATION NUMBER: 31,794
; REFERENCE/DOCKET NUMBER: UF35.1.FWCC1
```

; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 904-375-8100  
; TELEFAX: 904-372-5800  
; INFORMATION FOR SEQ ID NO: 28:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 236 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-307-499-28

Query Match 26.7%; Score 50.5; DB 1; Length 236;  
Best Local Similarity 42.3%; Pred. No. 4.3;  
Matches 11; Conservative 4; Mismatches 10; Indels 1; Gaps 1;

QY 1 VIFNYK-GKNVLINKDIRCKDDDEPHT 25  
DB 164 IINTYKEDTISINIRLCKCKDDIIKH 189

RESULT 5  
US-09-299-268-28  
; Sequence 28, Application US/09299268  
; Patent No. 6217882  
; GENERAL INFORMATION:  
; APPLICANT: Moyer, Richard W.  
; APPLICANT: Vi uela, Eladio  
; APPLICANT: Gibbs, E.P.J.  
; TITLE OF INVENTION: Use of Recombinant Swine Poxvirus as a  
; TITLE OF INVENTION: Live Vaccine Vector  
; NUMBER OF SEQUENCES: 60  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: David R. Saliwanchik  
; STREET: 2421 N.W. 41st Street, Suite A-1  
; CITY: Gainesville  
; STATE: Florida  
; COUNTRY: U.S.A.  
; ZIP: 32606  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/299,268  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/901,127  
; FILING DATE:  
; APPLICATION NUMBER: US 07/908,241  
; FILING DATE: 1-JUL-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/908,630  
; FILING DATE: 29-JUN-1992  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/342,212  
; FILING DATE: 21-APR-1992  
; CLASSIFICATION:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Saliwanchik, David R.  
; REGISTRATION NUMBER: 31,794  
; REFERENCE/DOCKET NUMBER: UF35.1.FWCCI  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 904-375-8100  
; TELEFAX: 904-372-5800  
; INFORMATION FOR SEQ ID NO: 28:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 236 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear

; MOLECULE TYPE: protein  
US-09-299-268-28

Query Match 26.7%; Score 50.5; DB 4; Length 236;  
Best Local Similarity 42.3%; Pred. No. 4.3;  
Matches 11; Conservative 4; Mismatches 10; Indels 1; Gaps 1;

QY 1 VIFNYK-GKNVLINKDIRCKDDDEPHT 25  
DB 164 IINTYKEDTISINIRLCKCKDDIIKH 189

RESULT 6  
US-08-996-679-63  
; Sequence 63, Application US/08996679  
; Patent No. 6169071  
; GENERAL INFORMATION:  
; APPLICANT: Blaschuk, Orest W.  
; APPLICANT: Gour, Barbara J.  
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING  
; TITLE OF INVENTION: CELL ADHESION  
; NUMBER OF SEQUENCES: 63  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: SEED and BERRY LLP  
; STREET: 6300 Columbia Center, 701 Fifth Avenue  
; CITY: Seattle  
; STATE: Washington  
; COUNTRY: USA  
; ZIP: 98104  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/996,679  
; FILING DATE: 23-DEC-1997  
; CLASSIFICATION:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Maki, David J.  
; REGISTRATION NUMBER: 31,392  
; REFERENCE/DOCKET NUMBER: 100086.401C1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (206) 622-4900  
; TELEFAX: (206) 682-6031  
; INFORMATION FOR SEQ ID NO: 63:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 17 amino acids  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: linear  
US-08-996-679-63

Query Match 25.4%; Score 48; DB 4; Length 17;  
Best Local Similarity 43.8%; Pred. No. 0.43;  
Matches 7; Conservative 7; Mismatches 2; Indels 0; Gaps 0;

QY 2 IFNYKGNVLINKDIR 17  
DB 1 IWKKGRDVLKDKVR 16

RESULT 7  
US-08-939-853A-14  
; Sequence 14, Application US/08939853A  
; Patent No. 6203788  
; GENERAL INFORMATION:  
; APPLICANT: Blaschuk, Orest W.  
; APPLICANT: Gour, Barbara J.  
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR REGULATING  
; TITLE OF INVENTION: CELL ADHESION

NUMBER OF SEQUENCES: 30  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: SEED and BERRY LLP  
STREET: 6300 Columbia Center, 701 Fifth Avenue  
CITY: Seattle  
STATE: Washington  
COUNTRY: USA  
ZIP: 98104  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/939,853A  
FILING DATE: 29-SEP-1997  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Maki, David J.  
REGISTRATION NUMBER: 32,391  
REFERENCE/DOCKET NUMBER: 100086.402  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (206) 622-4900  
TELEFAX: (206) 682-6031  
INFORMATION FOR SEQ ID NO: 14:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 17 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
US-08-939-853A-14

Query Match 25.4%; Score: 48; DB 4; Length 17;  
Best Local Similarity 43.8%; Pred. No. 0.43;  
Matches 7; Conservative 7; Mismatches 2; Indels 0; Gaps 0;

QY 2 IFNYKGKVNLINKDIR 17  
| : : | : : | : : | : : |  
DB 1 IWKKGRDVLKDKVR 16

RESULT 8  
US-09-115-395-23  
; Sequence 23, Application US/09115395A  
; Patent No. 6207639  
; GENERAL INFORMATION:  
; APPLICANT: Blaschuk, Orest W.  
; APPLICANT: Gour, Barbara J.  
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NEURITE OUTGROWTH  
; FILE REFERENCE: 100086.401C3  
; CURRENT APPLICATION NUMBER: US/09/115,395A  
; CURRENT FILING DATE: 1998-07-14  
; EARLIER APPLICATION NUMBER: 08/996,679  
; EARLIER FILING DATE: 1997-12-23  
; EARLIER APPLICATION NUMBER: 08/893,534  
; EARLIER FILING DATE: 1997-07-11  
; EARLIER APPLICATION NUMBER: 60/021,612  
; EARLIER FILING DATE: 1996-07-12  
; NUMBER OF SEQ ID NOS: 77  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 23  
; LENGTH: 17  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Solid Phase  
US-09-115-395-23

Query Match 25.4%; Score: 48; DB 4; Length 17;  
Best Local Similarity 43.8%; Pred. No. 0.43;

Matches 7; Conservative 7; Mismatches 2; Indels 0; Gaps 0;  
QY 2 IFNYKGKVNLINKDIR 17  
| : : | : : | : : | : : |  
DB 1 IWKKGRDVLKDKVR 16  
RESULT 9  
US-09-113-977C-68  
; Sequence 68, Application US/09113977C  
; Patent No. 6277824  
; GENERAL INFORMATION:  
; APPLICANT: Doherty, Patrick  
; APPLICANT: Blaschuk, Orest W.  
; APPLICANT: Gour, Barbara J.  
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING ADHESION MOLECULE  
; TITLE OF INVENTION: FUNCTION  
; FILE REFERENCE: 100086.403  
; CURRENT APPLICATION NUMBER: US/09/113,977C  
; CURRENT FILING DATE: 1998-07-10  
; NUMBER OF SEQ ID NOS: 87  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 68  
; LENGTH: 17  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Solid Phase  
US-09-113-977C-68

Query Match 25.4%; Score: 48; DB 4; Length 17;  
Best Local Similarity 43.8%; Pred. No. 0.43;  
Matches 7; Conservative 7; Mismatches 2; Indels 0; Gaps 0;

QY 2 IFNYKGKVNLINKDIR 17  
| : : | : : | : : | : : |  
DB 1 IWKKGRDVLKDKVR 16

RESULT 10  
US-08-752-238-3  
; Sequence 3, Application US/08752238  
; Patent No. 5804418  
; GENERAL INFORMATION:  
; APPLICANT: Lambowitz Dr., Alan M  
; APPLICANT: Mohr Dr., Georg  
; APPLICANT: Saldanha Dr., Roland  
; APPLICANT: Matsuura Dr., Manabu  
; TITLE OF INVENTION: Method for Preparing Nucleotide  
; TITLE OF INVENTION: Integrase  
; NUMBER OF SEQUENCES: 12  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: CALFEE, HALTER & GRISWOLD  
; STREET: 800 Superior Avenue  
; CITY: Cleveland  
; STATE: Ohio  
; COUNTRY: US  
; ZIP: 44114  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/752,238  
; FILING DATE:  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Goltick, Mary E.  
; REGISTRATION NUMBER: 34,829  
; REFERENCE/DOCKET NUMBER: 24671/00103

TELECOMMUNICATION INFORMATION:  
TELEPHONE: (216) 622-8458  
TELEFAX: (216) 241-0816  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 599 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-752-238-3

Query Match 24.9%; Score 47; DB 1; Length 599;  
Best Local Similarity 53.3%; Pred. No. 45;  
Matches 8; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 20 DDEFTHLYTLIVRPD 34  
|: || || :|||

Db 20 DEVFTRLRYLLRPD 34

RESULT 11  
US-09-085-603B-3  
Sequence 3, Application US/09085603B  
Patent No. 6001608  
GENERAL INFORMATION:  
APPLICANT: Lambowitz Dr., Alan M  
APPLICANT: Mohr Dr., Georg  
APPLICANT: Saldanha Dr., Roland  
APPLICANT: Matsuura Dr., Manabu  
APPLICANT: Yang Dr., Jiam  
APPLICANT: Zimmerly Dr., Steven  
APPLICANT: Guo Dr., Huatao  
APPLICANT: Beall Dr., Clifford J.  
TITLE OF INVENTION: Methods of Making an Rnp Particle  
TITLE OF INVENTION: Having Nucleotide Integrase Activity  
NUMBER OF SEQUENCES: 23  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: CALFEE, HALTER & GRISWOLD LLP  
STREET: 800 Superior Avenue  
CITY: Cleveland  
STATE: Ohio  
COUNTRY: US  
ZIP: 44114  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
FILING DATE:  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Docherty, Pamela A.  
REGISTRATION NUMBER: 40,591  
REFERENCE/DOCKET NUMBER: 24671/04000  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (216) 622-8416  
TELEFAX: (216) 241-0816  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 599 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-09-085-603B-3

Query Match 24.9%; Score 47; DB 3; Length 599;  
Best Local Similarity 53.3%; Pred. No. 45;  
Matches 8; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 20 DDEFTHLYTLIVRPD 34  
|: || || :|||

Db 20 DEVFTRLRYLLRPD 34

RESULT 12  
US-09-031-897-7  
Sequence 7, Application US/09031897  
Patent No. 6027895  
GENERAL INFORMATION:  
APPLICANT: Lambowitz, Alan  
APPLICANT: Mohr, Georg  
APPLICANT: Zimmerly, Steven  
APPLICANT: Guo, Huatao  
TITLE OF INVENTION: Methods Cleaving DNA with Nucleotide  
TITLE OF INVENTION: Integrases  
NUMBER OF SEQUENCES: 12  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Calfee, Halter & Griswold  
STREET: 800 Superior Avenue, Suite 1400  
CITY: Cleveland  
STATE: Ohio  
COUNTRY: US  
ZIP: 44114  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
FILING DATE:  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: Docherty, Pamela A.  
REGISTRATION NUMBER: 40,591  
REFERENCE/DOCKET NUMBER: 24671/00105  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (216) 622-8416  
TELEFAX: (216) 241 0816  
INFORMATION FOR SEQ ID NO: 7:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 599 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-09-031-897-7

Query Match 24.9%; Score 47; DB 3; Length 599;  
Best Local Similarity 53.3%; Pred. No. 45;  
Matches 8; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 20 DDEFTHLYTLIVRPD 34  
|: || || :|||

Db 20 DEVFTRLRYLLRPD 34

RESULT 13  
US-09-257-770-6  
Sequence 6, Application US/09257770  
Patent No. 6306596  
GENERAL INFORMATION:  
APPLICANT: Lambowitz, Allen M.  
APPLICANT: Zimmerly, Steven  
APPLICANT: Guo, Huatao  
APPLICANT: Mohr, Georg  
APPLICANT: Beall, Clifford J.  
TITLE OF INVENTION: Methods for Cleaving Single-Stranded and  
TITLE OF INVENTION: Double-Stranded DNA Substrates with Nucleotide  
TITLE OF INVENTION: Integrase  
FILE REFERENCE: 24671/04007  
CURRENT APPLICATION NUMBER: US/09/257,770

